

us-09-077-817-12.rag

Sat Sep 1 19:37:55 2001

GenCore version 4.5
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OM protein - protein search, using sw model
September 1, 2001, 19:16:53 ; search time 21.2 seconds
(without alignments)
Run on: 1080.937 Million cell updates/sec

Title: US-09-077-817-12
Perfect score: 2087
Sequence: 1 MAFVCLAIAGLYFLISTTF.....TGLLRKPNTPKRVRCVTL 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues 412676

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

| Database : | A_Geneseq_0601.* |
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| 2: | /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.* |
| 3: | /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.* |
| 4: | /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.* |
| 5: | /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.* |
| 6: | /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.* |
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| 11: | /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.* |
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| 13: | /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.* |
| 14: | /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.* |
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| 20: | /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.* |
| 21: | /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.* |
| 22: | /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Query Length | ID | Description |
|------------|-------|-------|--------------|----------|----------------------|
| 1 | 2059 | 98.7 | 380 | AAW24972 | Human interleukin-13 |
| 2 | 2059 | 98.7 | 380 | AAW35295 | Human IL-13 bindin |
| 3 | 2059 | 98.7 | 380 | AAW36613 | Human Zcytor2 cyto |
| 4 | 2059 | 98.7 | 380 | AAW41520 | Human HR-1 recepto |
| 5 | 2059 | 98.7 | 380 | AAW41502 | Human cytokine/pep |
| 6 | 2059 | 98.7 | 380 | AAW33603 | Homo sapiens HR-1 |
| 7 | 2059 | 98.7 | 380 | AAW35296 | IL-13 binding chai |
| 8 | 2059 | 98.7 | 380 | AAW72136 | Human interleukin |
| 9 | 2059 | 98.7 | 380 | AAW29748 | Human IL-13 recept |
| 10 | 2059 | 98.7 | 380 | AAW36614 | Human Zcytor2 cyto |
| 11 | 1853 | 88.8 | 372 | AAW36616 | Celebus macaque zc |

Mature interleukin
Construct containi
Murine IL-13 bindi
IL-13 binding chai
Murine interleukin
Mouse IL-13 recept
Interleukin-13 bin
Sequence of secret
Sequence of secret
Human interleukin-
Human IL-5 recepto
Sequence of human
Protein used in pr
Human interleukin-
Human interleukin-
Human interleukin-
Mouse interleukin-
IL5-R-GBP 130 fusi
Soluble human IL-5
shIL-5R-alpha. Sy
Human interleukin-
IL-13/IL-4 dual tr
Sequence of interl
Sequence of interl
Sequence of interl
Sequence of interl
Sequence of interl
IL-2 receptor gamm
IL-2 receptor gamm
Murine IL-2R gamma
Human cytokine rec

| | | | | | |
|----|--------|------|------|----|----------|
| 12 | 1753 | 84.0 | 315 | 19 | AAW56261 |
| 13 | 1753 | 84.0 | 359 | 19 | AAW56260 |
| 14 | 1194.5 | 57.2 | 383 | 18 | AAW35294 |
| 15 | 1194.5 | 57.2 | 383 | 21 | AAW35295 |
| 16 | 1194.5 | 57.2 | 383 | 22 | AAW72135 |
| 17 | 1194.5 | 57.2 | 383 | 22 | AAW29747 |
| 18 | 456 | 21.8 | 157 | 19 | AAW56252 |
| 19 | 310.5 | 14.9 | 396 | 13 | AAW22216 |
| 20 | 310.5 | 14.9 | 396 | 13 | AAW22220 |
| 21 | 310.5 | 14.9 | 420 | 13 | AAW22219 |
| 22 | 310.5 | 14.9 | 420 | 19 | AAW82842 |
| 23 | 309.5 | 14.6 | 421 | 13 | AAW25064 |
| 24 | 304.5 | 14.2 | 420 | 13 | AAW22215 |
| 25 | 297 | 14.0 | 313 | 18 | AAW21856 |
| 26 | 294.5 | 14.1 | 427 | 18 | AAW24973 |
| 27 | 294.5 | 14.1 | 427 | 22 | AAW19807 |
| 28 | 293.5 | 14.1 | 426 | 18 | AAW09822 |
| 29 | 292.5 | 14.0 | 426 | 18 | AAW09821 |
| 30 | 292.5 | 14.0 | 1026 | 16 | AAW70121 |
| 31 | 292 | 14.0 | 335 | 13 | AAW25063 |
| 32 | 285.5 | 13.7 | 335 | 14 | AAW33699 |
| 33 | 285 | 13.6 | 793 | 21 | AAW92207 |
| 34 | 284 | 13.6 | 784 | 21 | AAW92208 |
| 35 | 284 | 11.6 | 398 | 13 | AAW22212 |
| 36 | 241 | 11.5 | 415 | 13 | AAW22217 |
| 37 | 241 | 11.5 | 415 | 13 | AAW22214 |
| 38 | 229 | 11.0 | 315 | 13 | AAW22213 |
| 39 | 229 | 11.0 | 332 | 13 | AAW22218 |
| 40 | 229 | 11.0 | 332 | 13 | AAW22218 |
| 41 | 229 | 10.5 | 369 | 15 | AAW47148 |
| 42 | 219 | 10.5 | 347 | 15 | AAW47149 |
| 43 | 209.5 | 10.0 | 369 | 15 | AAW59094 |
| 44 | 209 | 10.0 | 482 | 19 | AAW31646 |

ALIGNMENTS

| RESULT | 1 |
|----------|---|
| AAW24972 | AAW24972 standard; protein; 380 AA. |
| ID | AAW24972 |
| XX | AAW24972; |
| AC | 22-JUN-1998 (first entry) |
| DT | Human interleukin-13 beta receptor. |
| DE | Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13. |
| DE | Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13. |
| KW | Homo sapiens. |
| OS | WO9720926-A1. |
| PN | 12-JUN-1997. |
| PD | 07-NOV-1996; 96WO-FR01756. |
| XX | 06-DEC-1995; 95FR-0014424. |
| XX | (SNFI) SANOFI SA. |
| XX | Caput D, Ferrara P, Laurent P, Vita N; |
| XX | WPI: 1997-319773/29. |
| XX | N-PSDB: AAT85826, AAT86464. |
| DR | New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy, etc |
| PT | Claim 1; Figure 2a; 83pp; French. |
| XX | |
| PS | |

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R
 CC and alpha which can be used as IL-13 antagonists specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX
 SQ Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 18; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLISTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
 Db 1 mafvclaigcltyflistfgctssdteikvnpqdfeidvdpgylylqwqpplsl 60
 QY 61 HFKECTVEYELKYNIGSEWTKILNHYKDGFDLNGKTEAKTHLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwkilcnhykgdgdlnkgleakihllpwqctngse 120
 QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWOYLCSWKPGIGVLLDPNNLYFYWEGLDH 180
 Db 121 sswaettywispigipetkvdmdcvynnwylcswkpgigvlldpnnlyfywegli 180
 QY 181 ALOQVDYIKADGNTGCRPPYLEASDYKDFYICVNGSENKPIRSSYFFFOQNTVKPLP 240
 Db 181 alqcvdyikadgngcrfpyleasykdfyicvngssenkprrsyfffoqntvkpl 240
 QY 241 PVLNFTRESSCEIKLWSIPLGPAPCFDYEIREDDTTLVTATVENETYLKTTNE 300
 Db 241 pylvnftressceiklwsiplgpapcfdyeireddttlvtatvenetylktne 300
 QY 301 TRLQCFVRSKVNLYCSDGINSWSKOCWEGEDLSKTLRLFWLPFGPILILVIFVTG 360
 Db 301 trlqcfvrskvnlycsdgiwsewskgcwgedlskttlrlfwlpfgpililvifv 360
 QY 361 LLLRKPNTPKMW 373
 Db 361 llrkpnktpkmi 373

RESULT 2

AAW35295
 ID AAW35295 standard; Protein; 380 AA.
 XX
 AC AAW35295;
 XX
 DT 27-MAR-1998 (first entry)
 DE Human IL-13 binding chain of the IL-13 receptor.
 XX Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.
 XX

OS Homo sapiens.
 XX Key
 FH Peptide
 FT Location/Qualifiers
 FT 1..25
 FT /label= signal_sequence
 FT 26..380
 FT /note= "putative"
 FT Protein
 FT Domain
 FT /label= mature_protein
 FT 26..341
 FT /label= extracellular_domain
 FT 342..362
 FT /label= transmembrane_domain
 FT 363..380
 FT /label= intracellular_domain
 XX WO9731946-A1.
 XX 04-SEP-1997.
 XX 28-FEB-1997; 97WO-US03124.
 XX 01-MAR-1996; 96US-0609572.
 XX (GENY) GENETICS INST INC.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;
 XX WPI; 1997-448632/41.
 XX N-PSDB; AAT95214.
 XX New nucleic acid encoding interleukin-13 receptor binding chain and
 XX transformed cells - proteins antibodies and inhibitors, for
 XX treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 XX and in diagnosis
 PS Claim 11; Pages 34-35; 49pp; English.
 CC The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor,
 CC other than IL-13bc, IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.
 CC
 SQ Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 18; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLISTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
 Db 1 mafvclaigcltyflistfgctssdteikvnpqdfeidvdpgylylqwqpplsl 60
 QY 61 HFKECTVEYELKYNIGSEWTKILNHYKDGFDLNGKTEAKTHLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwkilcnhykgdgdlnkgleakihllpwqctngse 120
 QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWOYLCSWKPGIGVLLDPNNLYFYWEGLDH 180
 Db 121 sswaettywispigipetkvdmdcvynnwylcswkpgigvlldpnnlyfywegli 180

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QY 181 ALQCVDIKADQNGICRFPYLEASDKYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
Db 181 alqcvdyikadqngicrfyleasdkfyicvngssenkiprissyftfqlqnvkplp 240
QY 241 PVIYTFRESSCEIKLWSIPLGPIPARCFDYETEIREDDTTLVATVENETYTLKTNE 300
Db 241 pviytfressceiklwsiplgpiparcfdyeteireddttlvtatvenetytlktne 300
QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKTKLLRFLWLPFGFILLIVIFVTG 360
Db 301 trqlcfvvrskvnlycsddgiwsewskqwegedlsktkllrflwlpfgfllilvifvtg 360
QY 361 LLLRKPNTYPKMW 373
Db 361 llrrkpnypkmi 373

RESULT 3
AAW36613
ID AAW36613 standard; Protein; 380 AA.
XX AC AAW36613;
XX DT
XX DE Human Zcytor2 cytokine receptor protein.
XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 340..363
XX FT /label= transmembrane_domain
XX FT Domain 364..380
XX FT /label= intracellular_domain
XX FT Domain 25..339
XX FT /label= ligand_binding_domain
XX PN W09733913-A1.
XX PD 18-SEP-1997.
XX PF 12-MAR-1997; 97WO-US04043.
XX PR 13-MAR-1996; 96US-0013345.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
XX PI O'Hara PU;
XX DR WPI; 1997-470820/43.
XX DR N-PSDB; AAT96782.
XX DT New nucleic acid encoding testis-specific cytokine receptor - useful
XX PT for identification of ligands or antagonists, potentially for use as
XX PT male contraceptives or for infertility treatment
XX PS Claim 2; Page 47-48; 79pp; English.
XX CC This sequence represents a novel ligand-binding receptor, Zcytor2,
XX CC which shares homology with cytokine receptors and was isolated from human
XX CC placental polyA+ RNA. The resulting polypeptide is a receptor for
XX CC cytokines (particularly interleukin-13) and is expressed on the surface
XX CC of testicular cells, probably being involved in spermatogenesis. It can
XX CC be used to detect ligands that promote proliferation and/or
XX CC differentiation of such cells in cultures and may also be used to treat
XX CC infertility. Antagonists of this receptor may be used to characterise
XX CC ligand-receptor interactions and as male-specific contraceptives. By
XX CC blocking the action of IL-13, receptor antagonists and ligand-binding
XX CC this receptor can also be used to modulate immune function, e.g. in
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CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX SQ Sequence 380 AA;
Query Match 98.7%; Score 2059; DB 18; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTFELISTTFCGTSSTDEIKVNPDPQDFEIVDPGYLGYLYLQWQPPISLD 60
Db 1 mafvclaigclytfelisttfgctssstdeikvnpdpqdfelvdpgylglylylqwppisld 60
QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNKGEAKIHTLLPQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktliitknlhykdgfdlnkgeakihltllpwqctngsevg 120
QY 121 SSWAETTYWISPGQIPETKVQDMDCVYNNWOYLLCSNKPQIGVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispgqipetkvqdmcdvynnwoyllcsnkpqigvlldtynnlfywegldh 180
QY 181 ALQCVDIKADQNGICRFPYLEASDKYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
Db 181 alqcvdyikadqngicrfyleasdkfyicvngssenkiprissyftfqlqnvkplp 240
QY 241 PVIYTFRESSCEIKLWSIPLGPIPARCFDYETEIREDDTTLVATVENETYTLKTNE 300
Db 241 pviytfressceiklwsiplgpiparcfdyeteireddttlvtatvenetytlktne 300
QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKTKLLRFLWLPFGFILLIVIFVTG 360
Db 301 trqlcfvvrskvnlycsddgiwsewskqwegedlsktkllrflwlpfgfllilvifvtg 360
QY 361 LLLRKPNTYPKMW 373
Db 361 llrrkpnypkmi 373

RESULT 4
AAW41520
ID AAW41520 standard; Protein; 380 AA.
XX AC AAW41520;
XX DT 22-JUN-1998 (first entry)
XX DE Human HR-1 receptor.
XX KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
XX KW haematopoietic disorder; tumour; therapy; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT /label= Sig_peptide
XX FT Protein 22..380
XX FT /label= Mat_protein
XX PN W09747741-A1.
XX PD 18-DEC-1997.
XX PR 12-JUN-1996; 96WO-US10262.
XX PR 12-JUN-1996; 96WO-US10262.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
```

XX PI Appelbaum ER, Hu J;
XX KW WPI: 1998-052308/05.
DR N-PSDB; AAV04131.
XX
XX Nucleic acid sequence encoding human cytokine peptide hormone
PT receptor - useful to treat, prevent or diagnose, e.g. lowered
PT resistance to infection, asthma, allergy or haematopoietic disease
XX
XX Claim 13; Page 62-64; 76pp; English.
XX
XX This protein comprises a novel human cytokine/peptide hormone
CC receptor, designated the HR-1 receptor, that shows 27% identity
CC and 52% similarity to the interleukin-5 receptor. Its amino acid
CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
CC human testis library. Recombinant HR-1 receptor can be expressed
CC in claimed host cells, and used in a claimed method for identifying
CC compounds which bind to, and activate or inhibit, it. HR-1
CC receptor activators and agonists can be used to treat, prevent or
CC diagnose predisposition to lowered resistance to infection, asthma,
CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
CC aplastic anaemia, neutropaenia or cytotoxic treatments for cancer.
CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
CC be used to treat conditions associated with HR-1 receptor
CC overexpression. The antibodies can also be used to determine HR-1
CC receptor levels, since overexpression may be diagnostic of tumours.
XX
XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 19; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTTFCGTSSTDEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60
Db 1 mafvclaigcltytlsttfgtssstdeikvnpqdfeidvpgylglylylqwpplsl 60
Qy 61 HFKECTVEYELKYRNIGSETWKTITKNLHYKDGFDLNKGIEAKIHLLPWQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktitknlykdgfdlnkgieakihllpwqctngsevg 120
Qy 121 SSWAETTYWISPGQIPETKVDMDCVYYNWOYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
Db 121 sswaettywispqgipetkvdmdcvynwqyllcswkpgigvlldtynlfnlyfwyegldh 180
Qy 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkpirssyftfqlqnvkplp 240
Qy 241 PVLTLFTRESSCEIKLWSIPLGPAPCFDYEIEIRDDTLTATVENETYTLKTNE 300
Db 241 pvltlftressceiklwsipigpfpapcfdyeiieirddtlvtavenetytlktne 300
Qy 301 TRQLCFVVRKVNIVYCSDDGIWSEWSKQCEGEDLKKTLRLFWLPFGFTLILVIFVTG 360
Db 301 trqlcfvvrskvnivcsddgiwsewsdkqcegedlkktlrlfwlpfgftlilvifvtg 360
Qy 361 LLLRKNPTNPKW 373
Db 361 llrlkpnptypkmi 373

RESULT 5
AAW41502
ID AAW41502 standard; Protein; 380 AA.
XX
XX AAW41502;
XX AC
XX DT 08-JUN-1998 (first entry)
XX DE Human cytokine/peptide receptor, HR-1 receptor.

XX
KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
KW neutropaenia; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= Sig_peptide
FT Protein 22..380
FT /label= Mat_protein
FT /note= "Claim 14"
XX
XX EP812913-A2.
XX
XX 17-DEC-1997.
XX
XX 04-JUN-1997; 97EP-0303815.
XX
XX 12-JUN-1996; 96US-0017843.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Appelbaum ER, Hu J;
XX
XX WPI: 1998-034974/04.
DR N-PSDB; AAV04075.
XX
XX Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
PT increase resistance to infections in individuals with trauma and/or
PT burns
XX
XX Claim 13; Page 27-28; 34pp; English.
XX
XX This protein comprises a novel human cytokine/peptide hormone
CC receptor, designated HR-1 receptor. The amino acid sequence
CC was deduced from a cDNA clone (see AAV04075) isolated from a human
CC testis cDNA library. It shows 27% amino acid identity and 52%
CC similarity with the human interleukin-5 receptor. Also claimed are
CC polynucleotides encoding HR-1 receptor, vector and host cells, an
CC antagonist to the polypeptide, antibody against the polypeptide, an
CC antagonist that inhibits the activity of the polypeptide, a process
CC for diagnosing a disease, or a susceptibility to disease, related
CC to expression of HR-1 receptor, and a method for identifying
CC compounds that activate or inhibit the HR-1 receptor. HR-1
CC receptor protein and polynucleotides can be used for research,
CC biological, diagnosis and (gene) therapy applications, e.g. to
CC increase resistance to infections in individuals with trauma and/or
CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
CC predisposition to asthma, allergic disorders or disorders of
CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
CC cyclic neutropaenia or as a consequence of cytotoxic therapy of
CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.
XX
XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 19; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTTFCGTSSTDEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60
Db 1 mafvclaigcltytlsttfgtssstdeikvnpqdfeidvpgylglylylqwpplsl 60
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Qy 121 SSWAETTYWISPGQIPETKVDMDCVYYNWOYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
Db 121 sswaettywispqgipetkvdmdcvynwqyllcswkpgigvlldtynlfnlyfwyegldh 180

Db 121 sswaettywispqgipetkvqmdcvynwqyllicswkpgigvlltdnynlfywyegldh 180
Qy 181 ALQCVDYIKADGQNGRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadgqngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDDDTLTATVENETYTLKTTNE 300
Db 241 pvyltftressceiklwsipglpiparcfdyeieirdddtltatvenetytlktne 300
Qy 301 TRQLCFVVRSKVNIYCSDDGIWSWSKQCEGDELKSKTLLRFWLPFGFLLILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsesdkqcegedlkskllrlfwlpfgfllilvifvtg 360
Qy 361 LLRKPNTPYKMW 373
Db 361 llrkpntpykmi 373

RESULT 6
AAW33603
ID AAW33603 standard; Protein; 380 AA.
XX AC AAW33603;
XX DT 08-JUN-1998 (first entry)
XX XX Homo sapiens HR-1 receptor.
XX KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;
XX KW syndrome; aplastic anaemia; neutropaenia; cancer treatment;
XX KW infection resistance; diagnosis; tumours; HR-1 receptor;
XX KW asthma; allergic; haematopoietic; disorder.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
XX W09747742-A1.
XX PD 18-DEC-1997.
XX XX 09-JUL-1996; 96WO-US11459.
XX PF 12-JUN-1996; 96WO-US10262.
XX PR 12-JUN-1996; 96US-0017843.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Appelbaum ER, Hu J;
XX XX WPI; 1998-052309/05.
XX DR N-PSDB; AAV02295.
XX XX DNA encoding human cytokine-peptide hormone receptor - useful for
XX PT treating preventing or diagnosing, e.g. lowered resistance to
XX PT infection, asthma, allergy, or haematopoietic disease
XX XX Claim 15; Fig 1; 75pp; English.
XX XX The sequence is that of the human cytokine/peptide hormone receptor
XX CC (HR-1 receptor). This, or it's activators or agonists, can be used to
XX CC treat, prevent or diagnose predisposition to lowered resistance to
XX CC infection, asthma, allergic or haematopoietic disorders, e.g. where
XX CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
XX CC neutropaenia or cytotoxic treatments for cancer. Antagonists of the
XX CC receptor, e.g. antibodies or fragments of it may be used to treat
XX CC conditions associated with overexpression of the HR-1 receptor, e.g.
XX CC those listed above. Antibodies may also be used to assay levels of HR-1
XX CC receptor, overexpression of which may be diagnostic of tumours, by usual

CC immunassays; to isolate and identify HR-1 receptor-expressing cells; or
CC for affinity purification of the HR-1 receptor.
XX SQ Sequence 380 AA;
Query Match 98.7%; Score 2059; DB 19; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIAGCLYTLISTFTGCTSSSTEIKVNPDPQFEIVDPGYLYLQWOPPLSLD 60
Db 1 mafvclaiagcllytlistftgctsssteikvnpdpqfeivdpgylylqwapplslid 60
Qy 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLKNKIEAKIHTLLPQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktititknlhykdgfdlnkgleakihltllpqctngsevq 120
Qy 121 SSWAETTYWISPOGIPETKVQMDCVYNNWQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispgipetkvqmdcvynwqyllicswkpgigvlltdnynlfywegldh 180
Qy 181 ALQCVDYIKADGQNGRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadgqngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDDDTLTATVENETYTLKTTNE 300
Db 241 pvyltftressceiklwsipglpiparcfdyeieirdddtltatvenetytlktne 300
Qy 301 TRQLCFVVRSKVNIYCSDDGIWSWSKQCEGDELKSKTLLRFWLPFGFLLILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsesdkqcegedlkskllrlfwlpfgfllilvifvtg 360
Qy 361 LLRKPNTPYKMW 373
Db 361 llrkpntpykmi 373

RESULT 7
AAW95296
ID AAW95296 standard; Protein; 380 AA.
XX AC AAW95296;
XX DT 12-SEP-2000 (first entry)
XX DE IL-13 binding chain of human IL-13 receptor.
XX KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
XX KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
XX KW immune complex disease; lupus; nephritis; thyroiditis;
XX KW Grave's disease; inflammatory; infection; therapy; antiallergic;
XX KW antiinflammatory; antiasthmatic; vaccine.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"
FT Protein 26..380
FT /note= "mature protein"
FT Domain 26..341
FT /note= "extracellular domain; a polypeptide
FT comprising amino acids 22-334 is
FT specifically claimed in Claim 11(e)"
FT Domain 342..362
FT /note= "transmembrane domain"
FT Domain 363..380
FT /note= "intracellular domain; a polypeptide
FT comprising amino acids 257-383 is
FT specifically claimed in Claim 11(f)"
XX XX

PN W0200036103-A1.
 XX 22-JUN-2000.
 XX 13-DEC-1999; 99WO-US29493.
 XX 14-DEC-1998; 98US-0211335.
 XX (GEM) GENETICS INST INC.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 PI Wills-Karp M;
 XX WPI: 2000-431587/37.
 XX N-PSDB; AAA27912.
 XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
 PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
 PT asthma, Grave's disease and inflammatory conditions of the lung -
 XX Claim 11(d); Page 53-54; 60pp; English.
 XX The present sequence is that of the interleukin-13 binding chain
 CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
 CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
 CC the haematopoietin receptor family that acts as a mediator of
 CC IL-13. The invention provides methods for the recombinant
 CC production of IL-13bc polypeptides, including claimed full-length
 CC IL-13bc, its extracellular domain, and its intracellular domain.
 CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
 CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
 CC of IL-13 and its receptor) can be used to treat conditions in
 CC which IL-13 is implicated, particularly IgE-mediated conditions and
 CC diseases including atopy, allergy, asthma, immune complex diseases
 CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
 CC thyroiditis and Grave's disease), lung inflammation,
 CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
 CC activation, IL-13bc proteins can also be used to enhance macrophage
 CC activation, e.g. in vaccination, treatment of mycobacterial or
 CC intracellular organisms or parasite infections. IL-13bc proteins
 CC may also be used to potentiate the effects of IL-13 in vitro and
 CC in vivo, as diagnostic agents, and to screen for agents capable of
 CC binding to IL-13bc or IL-13 receptor, or which interfere with the
 CC binding of IL-13 to its receptor.
 XX SQ Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 21; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLALGCLYTLSTTCTGCTSSDTEIKVNPQDPFEIVDPGLYLYLQWQPPPLSLD 60
 Db 1 mafvclalgclytlsttctgctssdteikvnpqdpfeivdpgllylylqwppplsl 60
 Qy 61 HFKECTVEYELKYNIGSETWKTITKLNHYKDGFDLNKGEAKIHTLLPQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitklnhykdgfdlnkgeakihtllpqctngsevq 120
 Qy 121 SSWAETTYWISPGQIPETKVQDMDCVYNNWQYLLCSMKPGIGVLLDTNLYFYWYEGLDH 180
 Db 121 sswaettywispgqipetkvqdmcdvynnwqyllcskpgigvlltdtnlyfywyegldh 180
 Qy 181 ALQCVDYIKADQNGICRFPYLEASDKDFYICVNGSENKPIRSSFTFQQLQNVKPLP 240
 Db 181 alqcvdyikadqngicrfpyleasdkdfyicvngssenkiprissyftfqlqnvkplp 240
 Qy 241 PVIYLTFTRESSCEIKLWSIPGLPIPARCFDYETEIREDDFTTLVATVENETYTLKTTNE 300
 Db 241 pviyftressceiklwsipglpiparcfdyeteireddfttlvatvenetytlktne 300

Qy 301 TRQLCFVVRSKVNIYCSDDGIWSEWSDKQWEGEDLSKKTLLRFLWLPFGFLILVIFVTG 360
 Db 301 trqlcfvvrskvniycsddgiwsewskqwegedlskktllrflwlpfgflilvifvtg 360
 Qy 361 LLRLKPNTPYKMW 373
 Db 361 llrlkpntpykmi 373
 RESULT 8
 AAY72136
 ID AAY72136 standard; Protein; 380 AA.
 XX AAY72136;
 XX 24-APR-2001 (first entry)
 DT Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
 XX Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
 KW therapy; tissue fibrosis; Schistosoma infection; surgical incision;
 KW cytostatic; wound; IL-13 related condition; allergic condition;
 KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
 KW macrophage activation.
 XX Homo sapiens.
 XX Location/Qualifiers
 FT Key 1..25
 FT Peptide /label= Signal_peptide
 FT Region 1..81
 FT /note= "this region is identical to the translated
 FT sequence of an expressed sequence tag (EST) identified
 FT as Y99f10.r1 human cDNA clone 41648 5"
 FT 26..380
 FT Protein /label= Mature_human_interleukin (IL)-13_binding_chain_
 FT of_IL-13_receptor
 FT 26..341
 FT Domain /note= "Extracellular domain; this region is specifically
 FT claimed in claims 1e, 6e, 15e and 23e"
 FT 342..362
 FT Domain /note= "Transmembrane domain"
 FT 363..380
 FT Domain /note= "Intracellular domain; this region is specifically
 FT claimed in claims 1f, 6f, 15f and 23f"
 XX W0200078336-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-US17103.
 XX 21-JUN-1999; 99US-0334512.
 XX (GEM) GENETICS INST INC.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 XX Wills-Karp M;
 XX WPI: 2001-080753/09.
 XX N-PSDB; AAD02335.
 XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
 PT in a mammalian subject, involves administering a pharmaceutical
 PT composition comprising IL-13 antagonist -
 XX Claim 1a; Page 69-70; 72pp; English.
 XX The invention relates to a method of treating, or inhibiting
 CC the formation of tissue fibrosis in mammals, which involves
 CC administering a pharmaceutical composition comprising interleukin
 CC (IL)-13 antagonist. The protein of the invention is useful for

treating tissue fibrosis resulting from infection with Schistosoma or from healing of a wound which is a surgical incision, or inhibiting formation of tissue fibrosis which affects tissues such as liver, skin epidermis and endodermis, muscle, tendon, cartilage, cardiac tissue, pancreas, lung, uterine tissue, neural tissue, testis, ovary, adrenal gland, artery, vein, colon, small intestine, biliary tract and gut. It is also used in the treatment or modulation of various IL-13 related conditions such as allergic conditions, nephrotic syndrome, thyroiditis, Grave's disease and cancer. The present sequence is human interleukin (IL)-13 binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used to potentiate the effects of IL-13. This protein is also used to enhance macrophage activation and hence can be used in vaccination or treatment of mycobacterial or parasitic infections.

XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 22; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
Db 1 mafvclaigcllytlsttfgctssdssteikvnpqdfvdpvglylylqwppplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktititknlykdgfdlnkgeakihltllpwqctngse 120

QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispgipetkvdmdcvynwqyllcswkpgigvlltdntynlfywegldh 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqngicrfyleasdykdfyicvngsenkpirssyftfqlnkvkplp 240

QY 241 PVIYFTFRESSCEIKLWSIPGLPIPARCFDYIEIRDDTTLVTATVENETYLKTTNE 300
Db 241 pviyftfressceiklwsipglpiparcfdyieirddttlvtatvenetyllktne 300

QY 301 TRQJCFVVRKVNICYSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFTLLILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlskttlrlfwlpgftllilvifvtg 360

QY 361 LLRRKPNTPYKMW 373
Db 361 llrrkpnlypkmi 373

RESULT 9
AAB29748
ID AAB29748 standard; Protein: 380 AA.

XX AC AAB29748;

XX XX 23-FEB-2001 (first entry)

XX DE Human IL-13 receptor IL-13 binding chain (IL-13bc).

XX KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnery;
KW wound healing; schistosoma infection; liver; skin; muscle;
KW cartilage; cardiac tissue; lung tissue; uterine tissue;
KW intestinal tissue; vascular tissue; neural tissue.

XX OS Homo sapiens.

XX PN WO200064944-A1.

XX XX 02-NOV-2000.

XX PD

PF 28-APR-2000; 2000WO-US11612.
XX PR
XX PR 28-APR-1999; 99US-0301808.
XX PA (GEMY) GENETICS INST INC.
XX XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
PI Whitters MJ, Wood C;
XX DR WPI: 2001-024676/03.
DR N-PSDB; AAC81416.
XX XX
XX XX Treating or inhibiting tissue fibrosis resulting from infection with
PT schistosoma and wound healing involves administering interleukin-13 or
PT interleukin-4 antagonist
XX XX
PS Claim 1; Page 76-77; 82pp; English.

XX The invention relates to a method of treating fibrosis in a mammal
CC by administering an interleukin-13 (IL-13) antagonist or an IL-4
CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding
CC chain (IL-13bc; AAB29748) of the IL-13 receptor (IL-13R), or
CC soluble fragments thereof. The method is useful for treating or
CC inhibiting the formation of tissue fibrosis resulting from the healing
CC of a wound, including a surgical incision wound, or from infection with
CC schistosoma. The method may be used to treat fibrosis in a variety of
CC tissues, particularly liver tissue, but also skin epidermis, skin
CC endodermis, muscle, tendon, cartilage, cardiac tissue, pancreatic
CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,
CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
CC tissue. The present sequence represents human IL-13bc.

XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 22; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
Db 1 mafvclaigcllytlsttfgctssdssteikvnpqdfvdpvglylylqwppplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktititknlykdgfdlnkgeakihltllpwqctngse 120

QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispgipetkvdmdcvynwqyllcswkpgigvlltdntynlfywegldh 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqngicrfyleasdykdfyicvngsenkpirssyftfqlnkvkplp 240

QY 241 PVIYFTFRESSCEIKLWSIPGLPIPARCFDYIEIRDDTTLVTATVENETYLKTTNE 300
Db 241 pviyftfressceiklwsipglpiparcfdyieirddttlvtatvenetyllktne 300

QY 301 TRQJCFVVRKVNICYSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFTLLILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlskttlrlfwlpgftllilvifvtg 360

QY 361 LLRRKPNTPYKMW 373
Db 361 llrrkpnlypkmi 373

RESULT 10
AAB36614
ID AAB36614 standard; Protein: 380 AA.

XX AC AAB36614;

XX 30-MAR-1998 (first entry)
XX Human Zcytor2 cytokine receptor protein.
XX
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX
XX Homo sapiens.
XX
XX WO9733913-A1.
XX
XX 18-SEP-1997.
XX
XX 12-MAR-1997; 97WO-US04043.
XX
XX 13-MAR-1996; 96US-0013345.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Farrah TM, Foster DC, Grant FU;
XX O'Hara PJ;
XX
XX WPI; 1997-470820/43.
XX N-PSDB; AAT96783.
XX
XX New nucleic acid encoding testis-specific cytokine receptor - useful
XX for identification of ligands or antagonists, potentially for use as
XX male contraceptives or for infertility treatment
XX
XX Claim 1; Page 51-53; 79pp; English.
XX
XX This sequence represents a novel ligand-binding receptor, Zcytor2, which
XX shares homology with cytokine receptors and was isolated from a human
XX testis cDNA library. The resulting polypeptide is a receptor for
XX cytokines (particularly interleukin-13) and is expressed on the surface
XX of testicular cells, probably being involved in spermatogenesis. It can
XX be used to detect ligands that promote proliferation and/or
XX differentiation of such cells in cultures and may also be used to treat
XX infertility. Antagonists of this receptor may be used to characterise
XX ligand-receptor interactions and as male-specific contraceptives. By
XX blocking the action of IL-13, receptor antagonists and ligand-binding
XX this receptor can also be used to modulate immune function, e.g. in
XX allergy and asthma, as a diagnostic to determine circulating levels of
XX ligand and also to isolate and purify ligands. Antibodies can be used to
XX assay circulating receptor (an abnormal level may be indicative of
XX disease such as cancer), for labelling cells that express the receptor,
XX and therapeutically as antagonist.
XX
XX Sequence 380 AA;

Query Match 97.48; Score 2033; DB 18; Length 380;
Best Local Similarity 98.94; Pred. No. 1.2e-190;
Matches 369; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLGICLYTLISTFCTSSDTEIKVNPDPQFEIVDPGVLGVLYIQWPPPLSLD 60
DB 1 mafvclgiclytlstfctssdteikvnpdpqfeivdpgvlylylqwpplsl 60
QY 61 HFKECTVEYELKYRNIGSETWTKTITIKNLHYKOGFDLNKGIEAKIHTLLPWCQTNGSEVQ 120
DB 61 hfkevtveyelkyrnisetwtkitknlykdgfdlnkgieakihcllpwqctngsevg 120
QY 121 SSWAETTYWISPGQIPETKVDQMCVYNNWQYLCSKWKPGIGVLLDNNYLFYWEGLDH 180
DB 121 sswaettywispqgipetkvdqmcvynnwqylcswkpgigvlltdnynlfwyegldl 180
QY 181 ALOQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFOLQNVKPLP 240
DB 181 alqcvdylkadqngicrfpyleasdykdfyicvngsgsenkpirssyftfqlqnvkplp 240
QY 241 PVYLTFTRESSCEIKLKWISPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTNE 300

DB 241 pvyltftressceiklkwisplgpiiparcfdyeieireddttlvtatvenetytlktne 300
QY 301 TROLCFVVRKSVNLYCSDDGITWSEMSDKQWEGEDLSKTKLLREWLPGFTLLILVIFVTG 360
DB 301 trqlcfvvrskvnlycsddgitwsemsdkqwegedlsktkllrflwplgftllilvifvtg 360
QY 361 LLRKPNNTYPKMV 373
DB 361 llrkpnntypkmi 373
RESULT 11
AAW36616
ID AAW36616 standard; Protein; 372 AA.
XX
XX AAW36616;
XX
XX 30-MAR-1998 (first entry)
XX Celebus macaque Zcytor2 protein.
XX
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX
XX Macaque sp.
XX
XX Key Location/Qualifiers
XX Protein i..372
XX FT /label= zcytor2
XX FT /note= "partial protein sequence"
XX
XX WO9733913-A1.
XX
XX 18-SEP-1997.
XX
XX 12-MAR-1997; 97WO-US04043.
XX
XX 13-MAR-1996; 96US-0013345.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Farrah TM, Foster DC, Grant FU;
XX O'Hara PJ;
XX
XX WPI; 1997-470820/43.
XX N-PSDB; AAT96784.
XX
XX New nucleic acid encoding testis-specific cytokine receptor - useful
XX for identification of ligands or antagonists, potentially for use as
XX male contraceptives or for infertility treatment
XX
XX Example 4; Page 56-57; 79pp; English.
XX
XX This sequence represents a novel ligand-binding receptor, Zcytor2,
XX which shares homology with cytokine receptors and is isolated from
XX testis tissue obtained from a Celebus macaque. The resulting polypeptide
XX is a receptor for cytokines (particularly interleukin-13) and is
XX expressed on the surface of testicular cells, probably being involved in
XX spermatogenesis. It can be used to detect ligands promoting proliferation
XX and/or differentiation of such cells in cultures and may also be used to
XX treat infertility. Antagonists of this receptor may be used to
XX characterise ligand-receptor interactions and as male-specific
XX contraceptives. By blocking the action of IL-13, receptor antagonists and
XX ligand-binding this receptor can also be used to modulate immune
XX function, e.g. in allergy and asthma, as a diagnostic to determine
XX circulating levels of ligand and also to isolate and purify ligands.
XX Antibodies can be used to assay circulating receptor (an abnormal level
XX may be indicative of disease such as cancer), for labelling cells that
XX express the receptor, and therapeutically as antagonist.
XX
XX Sequence 372 AA;

Query Match 88.8%; Score 1853; DB 18; Length 372;
Best Local Similarity 92.2%; Pred. No. 5e-173;
Matches 343; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCCLYTFLLSTFGCTSSDSTEIKVNPQDPFVIDPGYLGLYLQWQPPSLD 60
DB 1 mafvylairclctflsttfgytstsdteikvnpqdpfvidpgylglYLQWQPPSLD 60

QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLANKGIEAKHTLLPWQCTNGSEVQ 120
DB 61 nkectveylkynigsetwtiitknlhykdgfdlnkgieakhtllpwqctngsevg 120

QY 121 SSWAETTWISPGQIPERKVDMDCVYINWQYLLCSWRPGIGVLLDTNINLFYWYEGLDH 180
DB 121 sswaeatywispqgipetkvdmdcvynwqyllcswkpgigvlltdnynlfywyegldr 180

QY 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQQLNIVKPLP 240
DB 181 alqcvdyikvqgnlgrcfpylessdykdfyicvngssetkpirssytfqqlnivkplp 240

QY 241 PVLFTRESSCEIKLWSIPLGPAPARCFDYEIREDDTTLVTATVENETYLTKTNE 300
DB 241 pvlctctgeslyelkksiplgparcfyeyelredtdtlvtatvenetytlktne 300

QY 301 TRQLCFVVRKVNICYSDGIGWSEWSKQCEGDELKSKTLLRFLWLPFGFLLILVIFVTG 360
DB 301 trqlcfvvrskvnicycsdggigwsewsdkqceveelkktlllflpfgfllilvifvtg 360

QY 361 LLLRPNYIPKM 372
DB 361 lllckrdsypkm 372

RESULT 12
AAW56261
ID AAW56261 standard; Protein; 315 AA.
XX AC AAW56261;
XX DT 16-SEP-1998 (first entry)
XX DE Mature interleukin-13 binding protein.
XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.
XX OS Homo sapiens.
XX PN WO9810638-A1.
XX PD 19-MAR-1998.
XX PF 10-SEP-1997; 97WO-AU00591.
XX PR 27-FEB-1997; 97AU-0005374.
XX PR 10-SEP-1996; 96AU-0002262.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX DR N-PSDB; AAV22702.
XX DR WPI; 1998-207062/18.
XX PT New isolated interleukin-13 binding protein - used to develop
XX PT products for therapy e.g. for allergic conditions such as asthma or
XX PT for diagnosis or detection
XX PS Disclosure; Page 55-56; 69pp; English.
XX CC The IL-13 binding protein and related therapeutic molecules can be used
XX CC in the antagonism of at least one IL-13 activity. They can be used for

CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.

XX Sequence 315 AA;

Query Match 84.0%; Score 1753; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDPDFEIVDPGILYLYLQWQPPSLDHFKECTVEYELKYNIGSETWKTITKN 88
DB 1 eikvnpdpdfeidpgylglYLQWQPPSLDHFKECTVEYELKYNIGSETWKTITKN 88

QY 89 LHYKDGFDLNGKIEAKHTLLPWQCTNGSEVQSSWAETTWISPGIPETKVDMDCVY 148

DB 61 lhykdgfdlnkgieakhtllpwqctngsevgsswaettywispqgipetkvqmdcvy 120

QY 149 NWQYLLCSWKPGIGVLLDTNINLFYWYEGLDHALQCVDIKADGONICRFPYLEASDYK 208

DB 121 nwqyllcswkpgigvlltdnynlfywyegldhalqcvdiKadgqnlgrcfpyleasyk 180

QY 209 DFYICVNGSSENKPIRSSYTFQQLNIVKPLPPVYLTFTRESSCEIKLWSIPLGPAPAR 268

DB 181 dfyicvngssenkiprissytfqqlnivkplppvyltftressceiklwsiplgpar 240

QY 269 CFDEIREDDTTLVTATVENETYLTKTNETROLCFVVRKVNICYSDGIGWSEWSK 328

DB 241 cfdeyeireddttltatvenetytlktnetrqlcfvvrskvnicycsdggigwsewsdk 300

QY 329 QCWEGEDLSKKTLLR 343

DB 301 qcwegedlskktllr 315

RESULT 13

AAW56260

ID AAW56260 standard; Protein; 359 AA.

XX AC AAW56260;

XX DT 16-SEP-1998 (first entry)

XX DE Construct containing mature interleukin-13 binding protein.

XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.

XX OS Homo sapiens.

XX PN WO9810638-A1.

XX PD 19-MAR-1998.

XX PF 10-SEP-1997; 97WO-AU00591.

XX PR 27-FEB-1997; 97AU-0005374.

XX PR 10-SEP-1996; 96AU-0002262.

XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;

XX DR WPI; 1998-207062/18.

XX DR N-PSDB; AAV22701.

XX PT New isolated interleukin-13 binding protein - used to develop
XX PT products for therapy e.g. for allergic conditions such as asthma or
XX PT for diagnosis or detection

Example 14; Page 52-53; 69pp; English.

PS The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
SQ Sequence 359 AA;

Query Match 84.0%; Score 1753; DB 19; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.9e-163;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 EIKVNPQDFEIVDPGYLYLQWQPLSLDHPKCEVYELKYRNIGSETWTKTIITKN 88
Db |||||
QY 89 LHYKDFDLNGIEAKIHTILPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMCVY 148
Db |||||
QY 105 IYKDFGDLNGIEAKIHTILPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMCVY 164
Db |||||
QY 149 NWYLLCSWKPGIGVLLDTNLFYWEGLDHALQCVDIKADGONIGCRPPYLEASDYK 208
Db |||||
QY 209 DFYICVNGSSNKPIRSSYFTFQONIVKPLPPVYLTFTRESSCEIKLWSIPGIPAR 268
Db |||||
QY 225 DFYICVNGSSNKPIRSSYFTFQONIVKPLPPVYLTFTRESSCEIKLWSIPGIPAR 284
QY 269 CFDYETREDDTLVATVENYTLKTTNETQOLCFVBSKNVYCSDDGIWSESDK 328
Db |||||
QY 329 QWGEDLSKTKLLR 343
Db |||||

RESULT 14
AAW35294
ID AAW35294 standard; Protein; 383 AA.
AC AAW35294;
XX
XX 27-MAR-1998 (first entry)
DE Murine IL-13 binding chain of the IL-13 receptor.
KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
KW allergy; asthma; immune complex disorder.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= signal_sequence
FT /note= "putative"
FT 22..383
FT Protein
FT /label= mature_protein
FT 22..334
FT Domain
FT /label= extracellular_domain
FT 335..356
FT Domain
FT /label= transmembrane_domain
FT 357..383
FT Domain
FT /label= intracellular_domain
XX
PN W09731946-A1.

PD 04-SEP-1997.
XX
XX 28-FEB-1997; 97WO-US03124.
XX
XX 01-MAR-1996; 96US-0609572.
XX (GEMY) GENETICS INST INC.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
PI Wood C;
XX
XX WPI; 1997-448632/41.
DR N-PSDB; AAT75213.
XX
XX New nucleic acid encoding interleukin-13 receptor binding chain and
PT transformed cells - proteins, antibodies and inhibitors, for
PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
PT and in diagnosis
XX
XX Claim 11; Pages 30-31; 49pp; English.
XX
CC The present sequence represents the murine interleukin-13 (IL-13) binding
CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
CC mediator of the known biological activities of IL-13. Recombinant
CC IL-13bc proteins, and antibodies raised against them, are used to
CC inhibit the binding of IL-13 to its receptor. They are particularly used
CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
CC They are also used to treat immune deficiency (particularly in
CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
CC with such activity is combined with IL-13bc and the mixture applied,
CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
CC expression of IL-13, its receptor or binding chain, and to raise specific
CC antibodies which may be useful for treating some tumours.
XX
SQ Sequence 383 AA;

Query Match 57.2%; Score 1194.5; DB 18; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.4e-108;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
QY 1 MAFVCLAIGCLYTFLLISTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPLSLD 60
Db |||||
QY 1 mafv--hircfcilctitgys----leakvnpqdfellpdlgllgylqwkppvvie 54
Db |||||
QY 61 HFKECTVEYELKYRNIGSETWTKTIITKNLHYKDFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
Db |||||
QY 121 SSWAEFTYWTSPQIPETKVQDMCVYNNWQYLLCSWKPGIGVLLDTNLFYWEGLDH 180
Db |||||
QY 115 spwieasygisdegslctkldmkciyynwqylvcswkpgktvysdntnaffvegldh 174
QY 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSNKPIRSSYFTFQONIVKPLP 240
Db |||||
QY 175 alqcadyldhdeknvgcklnslsdssdykdfcivngsskileprrssytfvqlnkvplp 234
QY 241 PVYLTFTRESSCEIKLWSIPGIPARCFDYETREDDTLVATVENYTLKTTNE 300
Db |||||
QY 235 peflhisvensidirmkwstpggipprcycyeyelvireddiswesatdkndmkkrane 294
QY 301 TROLCFVVRSKNVIYCSDDGIWSEMSDKQWGEDLSKTKLLRFLWLPFGFTLLILVIFVTG 360
Db |||||
QY 295 sedlcffvrckvnlncaddgiwsewseeecwgytgdskii-fivpvcilffillilic 353
QY 361 LLLRKPNTPK 372
Db |||||
QY 354 livekeeptl 365

RESULT 15

AA95295
ID AA95295 standard; Protein: 383 AA.

XX
AC AA95295;

XX
DT 12-SEP-2000 (first entry)

XX
DE IL-13 binding chain of mouse IL-13 receptor.

XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.

XX
OS Mus musculus.

XX
FH Key Location/Qualifiers

FT Peptide 1..21 /note= "signal peptide"

FT Protein 22..383 /note= "mature protein"

FT Domain 22..334 /note= "extracellular domain; a polypeptide comprising amino acids 22-334 is specifically claimed in Claim 11(b)"

FT Domain 335..356 /note= "transmembrane domain"

FT Domain 357..383 /note= "intracellular domain; a polypeptide comprising amino acids 257-383 is specifically claimed in Claim 11(c)"

FT FT

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New polynucleotide encoding an interleukin-13 (IL-13) binding chain of an IL-13 receptor for treating IgE-mediated conditions, such as atopy, asthma, Grave's disease and inflammatory conditions of the lung - Claim 11(a); Page 50-51; 60pp; English.

The present sequence is that of the interleukin-13 binding chain (IL-13bc) of the murine IL-13 receptor, as deduced from an isolated C3H/Heu mouse thymus cDNA clone (see AAA27911). IL-13bc is a member of the haematopoietin receptor family that acts as a mediator of IL-13. The invention provides methods for the recombinant production of IL-13bc polypeptides, including claimed full-length IL-13bc, its extracellular domain, and its intracellular domain. IL-13bc polypeptides, particularly soluble IL-13bc polypeptides, and IL-13 receptor inhibitors (e.g. antagonists of the interaction of IL-13 and its receptor) can be used to treat conditions in which IL-13 is implicated, particularly IgE-mediated conditions and diseases including atopy, allergy, asthma, immune complex diseases (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis, thyroiditis and Grave's disease), lung inflammation, immunodeficiency, and cancer. Since IL-13 inhibits macrophage activation, IL-13bc proteins can also be used to enhance macrophage

CC activation, e.g. in vaccination, treatment of mycobacterial or
CC intracellular organisms or parasite infections. IL-13bc proteins
CC may also be used to potentiate the effects of IL-13 in vitro and
CC in vivo, as diagnostic agents, and to screen for agents capable of
CC binding to IL-13bc or IL-13 receptor, or which interfere with the
CC binding of IL-13 to its receptor.
XX
SQ Sequence 383 AA;

Query Match 57.28; Score 1194.5; DB 21; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.4e-108;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
Qy 1 MAFVCLAGLCYTLFTLSTGCTSSDPEIKVNPQDPDFEIVDPGVLYLQWQPPPLSLD 60
Db 1 mafv--hircclfcilctitgys----leikvnpqdfelidpdllylylqwkppvvie 54
Qy 61 HFECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLKNKIEAKIHTLLPQCTNGSEVQ 120
Db 55 kfgctleyelkyrnvdsdsktlttrnllykdgfdlnkglegktrthlsehtngsevg 114
Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYLLCSWKPGLVLLDTNYNLFYWEGLDH 180
Db 115 spwieasygisdegslctkldmkciyynwqylvcswkpgktvysdntnmtffwyegldh 174
Qy 181 ALQCVDIYKADGQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
Db 175 alqcadylqhdeknvgcklnldssdykdficvngssklepirssyvtvflqlnivkplp 234
Qy 241 PVYLFTRESSECEIKLWSIPGLGPIPARCFDYIEIREDDDTLTVATVENEYTLKTNE 300
Db 235 peflhisvensidirmkwstpggipprcycyvelvireddiswesatdkndmklrrane 294
Qy 301 TRQJCFVVRKVNICYSDDGIGWSEWSKQCEGEDLSKTKTLRFLWLPFGFILILVIFVTG 360
Db 295 sedicffvrckvniycaddgiwsewseeecwgytgpdkii-fivpvcilffillilic 353
Qy 361 LLRRKPNYPKM 372
Db 354 livekeepeptl 365

Search completed: September 1, 2001, 19:17:23
Job time: 30 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:53 ; Search time 12.28 Seconds
(without alignments)
633.807 Million cell updates/sec

Title: US-09-077-817-12
Perfect score: 2087
Sequence: 1 MAFVCLAIGCLYFLISTTF.....TGILLRKPNYPKMRVNTL 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 2059 | 98.7 | 380 | 1 US-08-609-572-4 | Sequence 4, Appli |
| 2 | 2059 | 98.7 | 380 | 4 US-08-841-751-4 | Sequence 4, Appli |
| 3 | 2059 | 98.7 | 380 | 4 US-08-846-340-4 | Sequence 4, Appli |
| 4 | 1194.5 | 57.2 | 383 | 1 US-08-609-572-2 | Sequence 2, Appli |
| 5 | 1194.5 | 57.2 | 383 | 4 US-08-841-751-2 | Sequence 2, Appli |
| 6 | 1194.5 | 57.2 | 383 | 4 US-08-846-340-2 | Sequence 2, Appli |
| 7 | 310.5 | 14.9 | 420 | 1 US-07-757-390-13 | Sequence 13, Appl |
| 8 | 310.5 | 14.9 | 420 | 1 US-08-442-282-13 | Sequence 13, Appl |
| 9 | 310.5 | 14.9 | 420 | 1 US-08-442-281-13 | Sequence 13, Appl |
| 10 | 310.5 | 14.9 | 420 | 2 US-08-939-727-13 | Sequence 13, Appl |
| 11 | 309.5 | 14.8 | 396 | 1 US-07-757-390-14 | Sequence 14, Appl |
| 12 | 309.5 | 14.8 | 396 | 1 US-08-442-282-14 | Sequence 14, Appl |
| 13 | 309.5 | 14.8 | 396 | 1 US-08-442-281-14 | Sequence 14, Appl |
| 14 | 309.5 | 14.8 | 396 | 2 US-08-939-727-14 | Sequence 14, Appl |
| 15 | 294.5 | 14.1 | 427 | 4 US-08-969-125-9 | Sequence 9, Appli |
| 16 | 293 | 14.0 | 313 | 3 US-08-836-561-106 | Sequence 106, App |
| 17 | 292 | 14.0 | 335 | 1 US-07-947-130-2 | Sequence 2, Appli |
| 18 | 292 | 14.0 | 335 | 1 US-08-421-822-2 | Sequence 2, Appli |
| 19 | 292 | 14.0 | 335 | 1 US-08-421-823-2 | Sequence 2, Appli |
| 20 | 241 | 11.5 | 398 | 1 US-07-757-390-6 | Sequence 6, Appli |
| 21 | 241 | 11.5 | 398 | 1 US-08-442-282-6 | Sequence 6, Appli |
| 22 | 241 | 11.5 | 398 | 1 US-08-442-281-6 | Sequence 6, Appli |
| 23 | 241 | 11.5 | 398 | 2 US-08-939-727-6 | Sequence 6, Appli |
| 24 | 241 | 11.5 | 415 | 1 US-07-757-390-5 | Sequence 5, Appli |
| 25 | 241 | 11.5 | 415 | 1 US-08-442-282-5 | Sequence 5, Appli |
| 26 | 241 | 11.5 | 415 | 1 US-08-442-281-5 | Sequence 5, Appli |
| 27 | 241 | 11.5 | 415 | 2 US-08-939-727-5 | Sequence 5, Appli |

| | | | | | |
|----|-------|------|-----|---------------------|--------------------|
| 28 | 229 | 11.0 | 315 | 1 US-07-757-390-8 | Sequence 8, Appli |
| 29 | 229 | 11.0 | 315 | 1 US-08-442-282-8 | Sequence 8, Appli |
| 30 | 229 | 11.0 | 315 | 1 US-08-442-281-8 | Sequence 8, Appli |
| 31 | 229 | 11.0 | 315 | 2 US-08-939-727-8 | Sequence 7, Appli |
| 32 | 229 | 11.0 | 332 | 1 US-07-757-390-7 | Sequence 7, Appli |
| 33 | 229 | 11.0 | 332 | 1 US-08-442-282-7 | Sequence 7, Appli |
| 34 | 229 | 11.0 | 332 | 1 US-08-442-281-7 | Sequence 7, Appli |
| 35 | 229 | 11.0 | 332 | 2 US-08-939-727-7 | Sequence 7, Appli |
| 36 | 229 | 11.0 | 335 | 1 US-07-947-130-3 | Sequence 3, Appli |
| 37 | 229 | 11.0 | 335 | 1 US-08-421-822-3 | Sequence 3, Appli |
| 38 | 229 | 11.0 | 335 | 1 US-08-421-823-3 | Sequence 3, Appli |
| 39 | 220 | 10.5 | 369 | 1 US-08-052-205-4 | Sequence 4, Appli |
| 40 | 220 | 10.5 | 369 | 1 US-08-595-974-4 | Sequence 4, Appli |
| 41 | 219 | 10.5 | 347 | 1 US-08-052-205-7 | Sequence 7, Appli |
| 42 | 219 | 10.5 | 347 | 1 US-08-595-974-7 | Sequence 7, Appli |
| 43 | 212.5 | 10.2 | 369 | 2 US-08-424-224-2 | Sequence 2, Appli |
| 44 | 212.5 | 10.2 | 369 | 5 PCT-US94-02891-69 | Sequence 69, Appli |
| 45 | 207 | 9.9 | 252 | 1 US-08-052-205-9 | Sequence 9, Appli |

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-572-4

Query Match 98.7% Score 2059; DB 1: Length 380;
Best Local Similarity 99.7%; Pred. No. 2.1e-203;
Matches 37; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYFLISTTFGTSSTTEIKVNPQDPFIVDPGYLYLQWQPLSLD 60

Db 1 MAFVCLAIGCLYTLSTTFCGCTSSSDTEIKVNPDPQFEIVDPGVLGYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVDMDCVYNNWQYLLCSKPKGIGVLLDNTNLYFWYEGLDH 180
Db 121 SSWAETTWISPOGIPETKVDMDCVYNNWQYLLCSKPKGIGVLLDNTNLYFWYEGLDH 180
Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLOQIVKPLP 240
Db 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLOQIVKPLP 240
Qy 241 PVYLTFRESSCEIKLWKSIPGLPIPARCFDYEIEIRDDDTLVATVATVENETYTLKTNE 300
Db 241 PVYLTFRESSCEIKLWKSIPGLPIPARCFDYEIEIRDDDTLVATVATVENETYTLKTNE 300
Qy 301 TRQLCFVVRKVNIVCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFGLILVIFVTG 360
Db 301 TRQLCFVVRKVNIVCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFGLILVIFVTG 360
Qy 361 LLRKPNTYPRKW 373
Db 361 LLRKPNTYPRKI 373

RESULT 2

US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-841-751-4

Query Match 98.7%; Score 2059; DB 4; Length 380;
Best Local Similarity 99.7%; Pred. No. 2.1e-203;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLSTTFCGCTSSSDTEIKVNPDPQFEIVDPGVLGYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLSTTFCGCTSSSDTEIKVNPDPQFEIVDPGVLGYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
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Db 121 SSWAETTWISPOGIPETKVDMDCVYNNWQYLLCSKPKGIGVLLDNTNLYFWYEGLDH 180
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Db 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLOQIVKPLP 240
Qy 241 PVYLTFRESSCEIKLWKSIPGLPIPARCFDYEIEIRDDDTLVATVATVENETYTLKTNE 300
Db 241 PVYLTFRESSCEIKLWKSIPGLPIPARCFDYEIEIRDDDTLVATVATVENETYTLKTNE 300
Qy 301 TRQLCFVVRKVNIVCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFGLILVIFVTG 360
Db 301 TRQLCFVVRKVNIVCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFGLILVIFVTG 360
Qy 361 LLRKPNTYPRKW 373
Db 361 LLRKPNTYPRKI 373

RESULT 3

US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

Query Match 98.7%; Score 2059; DB 4; Length 380;
Best Local Similarity 99.7%; Pred. No. 2.1e-203;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAFVCLAIGCLYTLFTISFGCTSSSDTEIKVNPQDPEIVDPGVLGYLYLQWQPPLSLD 60
DB 1 MAFVCLAIGCLYTLFTISFGCTSSSDTEIKVNPQDPEIVDPGVLGYLYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
DB 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
QY 121 SSWAETTWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGLDVTNLYNLFYWEGLDH 180
DB 121 SSWAETTWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGLDVTNLYNLFYWEGLDH 180
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFOLQNIIVKPLP 240
DB 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFOLQNIIVKPLP 240
QY 241 PVYLTFTRESCEIKLWSIPLGPIPARCFDYIEIREDDTTLVTATVENETYLTKTTNE 300
DB 241 PVYLTFTRESCEIKLWSIPLGPIPARCFDYIEIREDDTTLVTATVENETYLTKTTNE 300
QY 301 TRQLCFVVRKSNVYICSDDGWSESDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
DB 301 TRQLCFVVRKSNVYICSDDGWSESDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
QY 361 LLLRKPNTYPKMW 373
DB 361 LLLRKPNTYPKMI 373
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RESULT 4
US-08-609-572-2

Sequence 2, Application US/08609572
Patent No. 5710023

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-572-2

Query Match 57.2%; Score 1194.5; DB 1; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.6e-114;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

```
QY 1 MAFVCLAIGCLYTLFTISFGCTSSSDTEIKVNPQDPEIVDPGVLGYLYLQWQPPLSLD 60
DB 1 MAFV--HRCLOFLLCTITGVS-----LEIKVNPQDPEIVDPGVLGYLYLQWQPPLSLD 54
QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
DB 55 KFKGCTLEVELKYRNVSDSNKTIITRNLIVKDGFDLNGKIEGKIRTHLSEHCINGSEVQ 114
QY 121 SSWAETTWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGLDVTNLYNLFYWEGLDH 180
DB 115 SPWIEASVIGSDEGSLETKIQDMKCIYYNWQYLLCSWKPGLDVTNLYNLFYWEGLDH 174
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFOLQNIIVKPLP 240
DB 175 ALQCADYIQLHDEKNVGCNLSNDSYKDFYICVNGSKLEPIRSSYTFOLQNIIVKPLP 234
QY 241 PVYLTFTRESCEIKLWSIPLGPIPARCFDYIEIREDDTTLVTATVENETYLTKTTNE 300
DB 235 PEFLLHISVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDMKLKRANE 294
QY 301 TRQLCFVVRKSNVYICSDDGWSESDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
DB 295 SEDLCFFVRCKVNIYCADDGIWSESEECWEGYTGTPDSKII-FIVPVCPLFFILLLLC 353
QY 361 LLLRKPNTYPKM 372
DB 354 LIVEKEPEPTL 365
```

RESULT 5

US-08-841-751-2
Sequence 2, Application US/08841751
Patent No. 6214559

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/841,751
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELEPHONE: (617) 498-8224
TELEFAX: (617) 498-8224
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-841-751-2

Query Match 57.2%; Score 1194.5; DB 4; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.6e-114;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLATGCLYTLFTSTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWPPVSLD 60
Db 1 MAFV-HIRCLCFILLCTITGYS----LEIKVNPQDFEIVDPGVLGYLYLQWPPVIE 54
QY 61 HFKECTVEYELKYNIGSEWTKTITRNLYKDGFDLNGKIEAKIHTLLPQCTNGSEVQ 120
Db 55 KFGCTLEYELKYNVDSWTKTITRNLYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
QY 121 SSWAETTYWISPGQIPETKVDMDCVVYNNQYLLCSWKPGLVLDNTNLYFYWVEGLDH 180
Db 115 SPWIEASGIDSGESLETKIQDMKCIYNNQYLLCSWKPGLVLDNTNLYFYWVEGLDH 174
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSENKPIRSSYTFQLOQIVKPLP 240
Db 175 ALQCADYLQHDEKNGVCKLSNLDSSDYKDFYICVNGSKLEPIRSSYTFVQLOQIVKPLP 234
QY 241 PVYLTFTRESCEIKLWSIPGLPAPCRFDYEIREDDDTTLVTATVENTYTLKTTNE 300
Db 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLRRANE 294
QY 301 TROLCFVVRKVNICYSDGDIWSEMSDKOCWEGEDLSKKTLLRFLWLPFGFLLILVIFVTG 360
Db 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDSKII-FIVPVCLEFFILLLLLC 353
QY 361 LLRLKPNYTPKM 372
Db 354 LIVEKEPEPTL 365

RESULT 6
US-08-846-340-2
Sequence 2, Application US/08846340
Patent No. 6248714
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whittiers, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELEPHONE: (617) 498-8224
TELEFAX: (617) 498-8224
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-2

Query Match 57.2%; Score 1194.5; DB 4; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.6e-114;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
QY 1 MAFVCLATGCLYTLFTSTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWPPVSLD 60
Db 1 MAFV-HIRCLCFILLCTITGYS----LEIKVNPQDFEIVDPGVLGYLYLQWPPVIE 54
QY 61 HFKECTVEYELKYNIGSEWTKTITRNLYKDGFDLNGKIEAKIHTLLPQCTNGSEVQ 120
Db 55 KFGCTLEYELKYNVDSWTKTITRNLYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
QY 121 SSWAETTYWISPGQIPETKVDMDCVVYNNQYLLCSWKPGLVLDNTNLYFYWVEGLDH 180
Db 115 SPWIEASGIDSGESLETKIQDMKCIYNNQYLLCSWKPGLVLDNTNLYFYWVEGLDH 174
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSENKPIRSSYTFQLOQIVKPLP 240
Db 175 ALQCADYLQHDEKNGVCKLSNLDSSDYKDFYICVNGSKLEPIRSSYTFVQLOQIVKPLP 234
QY 241 PVYLTFTRESCEIKLWSIPGLPAPCRFDYEIREDDDTTLVTATVENTYTLKTTNE 300
Db 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLRRANE 294
QY 301 TROLCFVVRKVNICYSDGDIWSEMSDKOCWEGEDLSKKTLLRFLWLPFGFLLILVIFVTG 360
Db 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDSKII-FIVPVCLEFFILLLLLC 353
QY 361 LLRLKPNYTPKM 372
Db 354 LIVEKEPEPTL 365

RESULT 7
US-07-757-390-13
Sequence 13, Application US/07757390
Patent No. 5453491
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomimaga, Akira
APPLICANT: Takagi, Satoshi

```

; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-757-390-13

```

```

Query Match      14.98; Score 310.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 1.3e-23;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

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Qy 27 DTEIKVNPQDFEIVDPGLGYLQWOPPLSLDHFKECTVEYELKYRNIGSETWTKITIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLPPVNFETKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 87 KNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKYQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAELH-APPGSPGTSVNNLTCT 135
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNNTNLFY---WYEGLDHALQCVDYIKAD 191
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTTDDNYSLRYSQVSLHCTWLVTGTDAPEDTQVFLYRYGSWTE-----ECQEYSKDT 189
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLNIVKPLPPVLTFTFR 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFPFTFISLKGDRWLAVLVNGSSKSHSAIRPFDQLFALHAIDQINPLNVTAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 249 ESSCEIKLWSIPLGPICPARCFDYEIEIREDDTTLVTATVENETTYLTKTNETRQLCFVW 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAPIHCFDYEIVKHNRNGYLOIEKLTWNAFISIDDLISKYDVQV 308
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 309 RSKVNIYCSDDGINSWSDKOCWEGEDLSKTKTLRFLWLPFGFILLVIFVFGLL 363
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS-QPIYYGVNDEHKP--LREW----FVIVINATICIFILL 356
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 8
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira

```

```

; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-282-13

```

```

Query Match      14.98; Score 310.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 1.3e-23;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

```

```

Qy 27 DTEIKVNPQDFEIVDPGLGYLQWOPPLSLDHFKECTVEYELKYRNIGSETWTKITIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLPPVNFETKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 87 KNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKYQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAELH-APPGSPGTSVNNLTCT 135
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNNTNLFY---WYEGLDHALQCVDYIKAD 191
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTTDDNYSLRYSQVSLHCTWLVTGTDAPEDTQVFLYRYGSWTE-----ECQEYSKDT 189
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLNIVKPLPPVLTFTFR 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFPFTFISLKGDRWLAVLVNGSSKSHSAIRPFDQLFALHAIDQINPLNVTAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 249 ESSCEIKLWSIPLGPICPARCFDYEIEIREDDTTLVTATVENETTYLTKTNETRQLCFVW 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAPIHCFDYEIVKHNRNGYLOIEKLTWNAFISIDDLISKYDVQV 308
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 309 RSKVNIYCSDDGINSWSDKOCWEGEDLSKTKTLRFLWLPFGFILLVIFVFGLL 363
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS-QPIYYGVNDEHKP--LREW----FVIVINATICIFILL 356
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 9
US-08-442-281-13
; Sequence 13, Application US/08442281

```

Patent No. 5807991
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-442-281-13

Query Match 14.9%; Score 310.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 1.3e-23;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;
QY 27 DTEIKVNPDPFEIVDPGYLYLQWOPPLSLDHFKRECTVEYELKYRNISETWTKIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYET 82
QY 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKVODMDCV 146
Db 83 ES---KCVTILHKGFSASVRILO---NDHSLASSWASAEHLH-APPGSGTGVNLTCT 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYFY----WYEGLDHALQCVDIKAD 191
Db 136 TTTEDNYSLRSYQVSLHCTWLVTGDPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSKNPKIRSYFTFQNLQNVKPLPPVYLFTTR 248
Db 190 LGRNIACWFPRTFILSKGRDLAVLVNGSSKHSAIRFPDQALFALHAIQDINPLNVTAEI 249
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVTATVENETTYTLKTTNETRQLCFVV 308
Db 250 EGT-RLSIQWEKPSAFPPIHCFDYEYKIHNRNGYLOIEKLMTNAFISIIDLSKYDVQV 308
QY 309 RSKYNIYSDGDIWSESDKOCWEGEDLSKTLRLFWLPFGFILLVIFVTGLL 363
Db 309 RAAVSSMCREAGLSEWS-QPIYVGNDEHKP--LREN----FVIVIMATCFILL 356

RESULT 10
US-08-939-727-13
Sequence 13, Application US/08939727
Patent No. 5916767
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,727
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-939-727-13

Query Match 14.9%; Score 310.5; DB 2; Length 420;
Best Local Similarity 27.9%; Pred. No. 1.3e-23;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;
QY 27 DTEIKVNPDPFEIVDPGYLYLQWOPPLSLDHFKRECTVEYELKYRNISETWTKIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYET 82
QY 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKVODMDCV 146
Db 83 ES---KCVTILHKGFSASVRILO---NDHSLASSWASAEHLH-APPGSGTGVNLTCT 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYFY----WYEGLDHALQCVDIKAD 191
Db 136 TTTEDNYSLRSYQVSLHCTWLVTGDPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSKNPKIRSYFTFQNLQNVKPLPPVYLFTTR 248
Db 190 LGRNIACWFPRTFILSKGRDLAVLVNGSSKHSAIRFPDQALFALHAIQDINPLNVTAEI 249
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVTATVENETTYTLKTTNETRQLCFVV 308
Db 250 EGT-RLSIQWEKPSAFPPIHCFDYEYKIHNRNGYLOIEKLMTNAFISIIDLSKYDVQV 308

DB 250 EGT-RLSIQWEKPVSAFFPIHCFDYEVKI

190 LGENTACWEPBTE

Db 250 EGT-RLSIQWEKP

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:24 ; Search time 24.79 seconds
(without alignments)
514.040 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372
Perfect score: 2056
Sequence: 1 MAFVCLAIGCLYFLISTTF.....ILVIFVTGLLRKPNTPK 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|--------------|--------------------|
| 1 | 2056 | 100.0 | 380 | 1 I132_HUMAN | Q14627 homo sapien |
| 2 | 309.5 | 15.1 | 420 | 1 IL5R_HUMAN | Q01344 homo sapien |
| 3 | 294.5 | 14.3 | 424 | 1 I131_MOUSE | O09030 mus musc |
| 4 | 294.5 | 14.3 | 427 | 1 I131_HUMAN | R78552 homo sapien |
| 5 | 261 | 12.7 | 831 | 1 PRLR_CHICK | Q04594 gallus gall |
| 6 | 241 | 11.7 | 415 | 1 IL5R_MOUSE | P21183 mus musc |
| 7 | 238 | 11.6 | 831 | 1 PRLR_MELGA | Q91094 meleagris g |
| 8 | 220 | 10.7 | 369 | 1 PRLR_HUMAN | P31785 mus sapien |
| 9 | 216.5 | 10.5 | 830 | 1 PRLR_COLLI | Q90374 columba liv |
| 10 | 212.5 | 10.3 | 369 | 1 CYRG_MOUSE | P34902 mus musc |
| 11 | 208 | 10.1 | 373 | 1 CYRG_CANFA | P40321 canis fam |
| 12 | 195 | 9.5 | 878 | 1 IL3B_MOUSE | P28954 mus musc |
| 13 | 189.5 | 9.2 | 379 | 1 CYRG_BOVIN | Q95118 bos taur |
| 14 | 178.5 | 8.7 | 897 | 1 CYRG_HUMAN | P32927 homo sapien |
| 15 | 173.5 | 8.4 | 896 | 1 CYRG_MOUSE | P26955 mus musc |
| 16 | 165 | 8.0 | 581 | 1 PRLR_BOVIN | Q28172 bos taur |
| 17 | 165 | 8.0 | 610 | 1 PRLR_RAT | P05710 rattus norv |
| 18 | 159 | 7.7 | 608 | 1 PRLR_MOUSE | Q08501 mus musc |
| 19 | 151 | 7.3 | 622 | 1 PRLR_HUMAN | P16471 homo sapien |
| 20 | 151 | 7.3 | 862 | 1 I12S_HUMAN | Q99665 homo sapien |
| 21 | 150.5 | 7.3 | 917 | 1 IL6B_MOUSE | Q00560 mus musc |
| 22 | 150 | 7.3 | 581 | 1 PRLR_CEREL | Q28235 cervus elap |
| 23 | 149 | 7.2 | 616 | 1 PRLR_RABIT | P14787 oryctolagus |
| 24 | 142.5 | 6.9 | 400 | 1 GCSR_HUMAN | P15509 homo sapien |
| 25 | 138 | 6.7 | 378 | 1 IL3R_HUMAN | P26951 homo sapien |
| 26 | 134.5 | 6.5 | 1097 | 1 LIFR_HUMAN | P42702 homo sapien |
| 27 | 131.5 | 6.4 | 630 | 1 PRLR_ORENT | Q91513 oreochromis |
| 28 | 128 | 6.2 | 874 | 1 I12S_MOUSE | P97378 mus musc |
| 29 | 126.5 | 6.2 | 918 | 1 IL6B_HUMAN | P40189 homo sapien |
| 30 | 120.5 | 5.9 | 836 | 1 GCSR_HUMAN | Q99062 homo sapien |
| 31 | 113.5 | 5.5 | 1165 | 1 LEPR_HUMAN | P48357 homo sapien |
| 32 | 112.5 | 5.5 | 1630 | 1 PTP1_DROME | P35992 drosophila |
| 33 | 109.5 | 5.3 | 918 | 1 IL6B_RAT | P40190 rattus norv |

RESULT 1

| | | | | |
|----|---|-----------|------|---------|
| ID | I132_HUMAN | STANDARD; | PRT; | 380 AA. |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) | | | |
| DE | INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 BINDING PROTEIN). | | | |
| GN | IL13RA2 OR IL13R. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Renal cell carcinoma; | | | |
| RX | MEDLINE=96279273; PubMed=8663118; | | | |
| RA | Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N., Ferrara P.; | | | |
| RA | "Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain.;" | | | |
| RL | J. Biol. Chem. 271:16921-16926(1996). | | | |
| RL | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Testis; | | | |
| RA | Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.; | | | |
| RL | Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Brain; | | | |
| RX | MEDLINE=973221053; PubMed=9177784; | | | |
| RA | Guo J., Aplou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.; | | | |
| RT | "Chromosome mapping and expression of the human interleukin-13 receptor.;" | | | |
| RL | Genomics 42:141-145(1997). | | | |
| CC | -!- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13), BUT NOT TO IL-4. | | | |
| CC | -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. | | | |
| CC | -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN. | | | |
| CC | -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. | | | |
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| CC | EMBL; X95302; CAA64617.1; ; | | | |
| DR | EMBL; U70981; AAB17170.1; ; | | | |
| DR | EMBL; Y08768; CAA70021.1; ; | | | |
| DR | MIM; 300130; ; | | | |

| | | | | | | |
|----|-------|-----|------|---|------------|--------------------|
| 34 | 107.5 | 5.2 | 638 | 1 | GHR_HUMAN | P10912 homo sapien |
| 35 | 107.5 | 5.2 | 837 | 1 | GCSR_MOUSE | P40223 mus musc |
| 36 | 107 | 5.2 | 634 | 1 | GHR_BOVIN | P79108 bos taur |
| 37 | 106 | 5.2 | 634 | 1 | GHR_SHEEP | Q28575 ovis aries |
| 38 | 105 | 5.1 | 511 | 1 | VGLG_VSVO | P04884 vesicular s |
| 39 | 104.5 | 5.1 | 1092 | 1 | LIFR_MOUSE | P19756 sus scrofa |
| 40 | 102.5 | 5.0 | 638 | 1 | GHR_PIG | P19941 oryctolagus |
| 41 | 101.5 | 4.9 | 638 | 1 | GHR_RABIT | Q62959 rattus norv |
| 42 | 99.5 | 4.8 | 1162 | 1 | LEPR_RAT | P16310 rattus norv |
| 43 | 99 | 4.8 | 638 | 1 | GHR_RAT | P48356 mus musc |
| 44 | 98.5 | 4.8 | 1162 | 1 | LEPR_MOUSE | P04883 vesicular s |
| 45 | 98 | 4.8 | 511 | 1 | VGLG_VSVIG | |

ALIGNMENTS

DR InterPro: IPR001777; -
 DR InterPro: IPR002465; -
 DR Pfam: PF00041; fn3; 1.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 380
 FT DOMAIN 27 343
 FT TRANSMEM 344 363
 FT DOMAIN 364 380
 FT DISULFID 145 155
 FT DISULFID 184 197
 FT CARBOHYD 115 115
 FT CARBOHYD 215 215
 FT CARBOHYD 290 290
 FT CARBOHYD 299 299
 SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;
 Query Match 100.0%; Score 2056; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 7.3e-161;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIICLTFLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLQWPPPLSLD 60
 Db 1 MAFVCLAIICLTFLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLQWPPPLSLD 60
 QY 61 HFKECTVEVELKYNIGSETWTKITITKNLHYKDGFDLNGKIEAKITHTLLPWQCTNGSEVQ 120
 Db 61 HFKECTVEVELKYNIGSETWTKITITKNLHYKDGFDLNGKIEAKITHTLLPWQCTNGSEVQ 120
 QY 121 SSWAETTYWISQGPETKVDQMDCVYVNWQVLLCSWPKGIGVLLDTNKNLFYWYEGLDH 180
 Db 121 SSWAETTYWISQGPETKVDQMDCVYVNWQVLLCSWPKGIGVLLDTNKNLFYWYEGLDH 180
 QY 181 ALQCVDYIKADGONIGCRPPYLEASDYKDFYICVNGSSNKPFRSSYFFQONIVKPLP 240
 Db 181 ALQCVDYIKADGONIGCRPPYLEASDYKDFYICVNGSSNKPFRSSYFFQONIVKPLP 240
 QY 241 PVLFTFTRESSCEIKLWSIPGLGPICPARCFDYEIETREDDTLVATVENETYLTKTNE 300
 Db 241 PVLFTFTRESSCEIKLWSIPGLGPICPARCFDYEIETREDDTLVATVENETYLTKTNE 300
 QY 301 TRLQCFVRSKNVNYCSDGIGWSESDKQWEGEDLSKKTLLRFLWLPFGFILLVIFVTG 360
 Db 301 TRLQCFVRSKNVNYCSDGIGWSESDKQWEGEDLSKKTLLRFLWLPFGFILLVIFVTG 360
 QY 361 LLRLKPNTYPMK 372
 Db 361 LLRLKPNTYPMK 372

RESULT 2
 IL5R_HUMAN STANDARD; PRT; 420 AA.
 ID IL5R_HUMAN
 AC Q01344;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).
 GN IL5RA OR IL5R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92372031; PubMed=1505961;
 RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
 RT "Structure and sequence of the human alpha-L-iduronidase gene.";
 RL Genomics 13:1311-1313(1992).
 [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92357767; PubMed=1495999;
 RA Tavernier J., Tuijens T., Plaetnick G., Verhee A., Fiers W.,
 RA Devos R.;
 RT "Molecular basis of the membrane-anchored and two soluble isoforms of the human interleukin 5 receptor alpha subunit.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
 [3]
 RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
 RX MEDLINE=92005669; PubMed=1833065;
 RA Tavernier J., Devos R., Cornelis S., Tuijens T., van der Heyden J.,
 RA Fiers W., Plaetnick G.;
 RT "A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-specific alpha chain and a beta chain shared with the receptor for GM-CSF";
 RL Cell 66:1175-1184(1991).
 CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN BINDS TO IL-5.
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/co/cdw125.htm".

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 DR EMBL; M96652; AAA59152.1; -
 DR EMBL; M96651; AAA59151.1; -
 DR EMBL; M75914; AAA36110.1; -
 DR EMBL; A26249; CAA01793.1; -
 DR EMBL; A24587; CAA01731.1; -
 DR EMBL; A26251; CAA01794.1; -
 DR PIR; A40267; A40267.
 DR MIM; 147851; -
 DR InterPro; IPR000950; -
 DR InterPro; IPR002465; -
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 420
 FT DOMAIN 21 342
 FT TRANSMEM 343 362
 FT DOMAIN 363 420
 FT CARBOHYD 35 35
 FT CARBOHYD 131 131
 FT CARBOHYD 216 216
 FT CARBOHYD 244 244
 FT VARSPPLIC 333 335
 FT VARSPPLIC 336 420
 FT VARSPPLIC 333 333
 FT VARSPPLIC 334 420
 SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;
 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 NDE -> FSR (IN SOLUBLE ISOFORM S1).
 MISSING (IN SOLUBLE ISOFORM S1).
 N -> K (IN SOLUBLE ISOFORM S2).
 MISSING (IN SOLUBLE ISOFORM S2).
 420681FBC6B51700 CRC64;

Query Match 15.1%; Score 309.5; DB 1; Length 420;
 Best Local Similarity 27.6%; Pred. No. 4.4e-18;
 Matches 98; Conservative 65; Mismatches 151; Indels 41; Gaps 15;
 QY 27 DTEIKVNPQDFEIVDPGVLGYLQWPPPLSLDFKCEVEYELKYNIGSETWTKIT 86
 Db 25 DEKISLPPNFTIKVTG-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPKEDDIETRI 82

RC TISSUE-B-cell;
RA Gauchat J.P.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
RA Eugster H.P., Bonnefoy J.Y.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-T-cell;
RX MEDLINE=97067184; PubMed=8910586;
RA Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
RA Leonard W.J.;
RA "cDNA cloning and characterization of the human interleukin 13
RT receptor alpha chain.";
RL J. Biol. Chem. 271:29265-29270(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
CC -!- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
CC SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
CC KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL; Y10659; CAA71669.1; -
DR EMBL; Y09328; CAA70508.1; -
DR EMBL; U62858; AAB37127.1; -
DR EMBL; U81379; AAD00510.3; -
DR HSP; P31785; 1ILN.
DR MIM; 300119; -
DR Interpro: IPR001777; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
KW SIGNAL 1 21
FT CHAIN 22 427
FT DOMAIN 22 343
FT TRANSMEM 344 367
FT DOMAIN 368 427
FT DOMAIN 39 102
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
FT CONFLICT 358 358
FT SEQUENCE 427 AA; 48759 MW; 5983B3E8F554107B CRC64;

Query Match 14.3%; Score 294.5; DB 1; Length 427;
Best Local Similarity 26.3%; Pred. No. 7.5e-17;
Matches 101; Conservative 59; Mismatches 161; Indels 63; Gaps 18;
QY 11 LYTELISITFTGCTSSDTEIKVPPQDFIVDPGLVLYLQWQPPPLSLDHFKECTVEY- 69
DB 10 LWALLCAGGGGGGGAAPTEPPVNLNLSVSNLCVTIWTNPPEGAS--SNCLWTF 67
QY 70 -----ELKYRNIGSETWTKITIKNLHYKDGFDLANKGIEAKIHTLLPWQC-TNGSEVOSSWA 124
DB 68 SHFGKQDKKIAPTRRSI-----EVLNERICLVGS---QCSTNESEKPSILV 114
QY 125 ETTYWIS-POGIPETKVQDMCVYNNQWYLLCSWPGICVLDTNLYNLFYETGDLHALQ 183
DB 115 EKC--ISPPEGPESAVTELOCIWHNLNLSYMKCSWLPGRNTSPDTNLYYHRSLEKIHQ 172
QY 184 CVDYIKADQONIGCFPPYLEASD--YKDFYICVNGSSSENKPIRSSVFTFOLQNIKPLPP 241
DB 173 C-ENIFREGQYGCDFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP 231
QY 242 --VYITFTRESSCEIKLWSPILGPPIPCFDFYIEIREDDT-----LYTATVENEY 293
DB 232 HIKLSFHD---DLVQWENPQNEI-SRCLFYEVVNSQTEHNVFYVQEAKECNPEF 287
QY 294 TLKTTNETRQLCFVY-----RSKNYIYC-SDDGIWSEMSDKQCEGEDLSKK 339
DB 288 ERNVENTS---CFWPGVLPDLNTVIRVKTNKLICYEDDKLWSNWSQEM-----SIGKK 339
QY 340 TLLRFLWPGFGLILVIFVTGLLL 363
DB 340 RNSTLYIT--MLLIVPVIVAGAI 361
RESULT 5
PRLR_CHICK STANDARD; PRT; 831 AA.
ID PRLR_CHICK
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RT the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; D13154; BAA02439.1; -
DR PIR; JQ1655; JQ1655.

DR HSP: P16471; lbp3.
DR InterPro: IPR000950; -
DR InterPro: IPR001777; -
DR InterPro: IPR002465; -
DR Pfam: PF00041; fn3; 4.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 123 225
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADBE9 CRC64;

Query Match 12.7%; Score 261; DB 1; Length 831;
Best Local Similarity 26.3%; Pred. No. 9.2e-14;
Matches 98; Conservative 55; Mismatches 175; Indels 44; Gaps 16;

QY 18 TFGCTSSDTEIKVN--PPQDFE---IVDPG-----YLGYLILQWOPPLSL 59
Db 97 TTFNITVATNEIGNSDPPQVDVTSIVQSPVNLFLTKRSANIMYLWAKWSPPLLA 156

QY 60 DHFKECTVEYELKYRNIGSEWTKITIKNLHKDGLNKGIEAKIHTLLPWOCTNGSEV 119
Db 157 DASSNHYELRIKPEKEWETI---SVGVQTOCKINR-LNAGMRVYVQVRCITLDGE 212

QY 120 QSSNAETTYWISPGQ-IPETKVQDMCVYNNQYLLCSWKPGIGVLLDTNNFLFYWYGL 178
Db 213 WSEWSERHILIPSQSPPEKPTIICRSPEKETFTCWKPGLDGCHPTNTLLYSKEGE 272

QY 179 DHALOCVDYIKADGONICRPPYLEADYKDFYICVNGSSSENKPIRSSYFFQLOQNIKVP 238
Db 273 EQVYECPDY-RTAGPN-SCYFDKKTSTFTYINITVTRATNEMGNSSDPHYVDVYIYQP 330

QY 239 LPPVYLTFTRSSCEIK----LKWS-IPGLPIPARCFDYEIEIR---EDDTTLVTATVEN 290
Db 331 DPPVNVTLLEKPKINRKYVLVLTWSPPLADVRSGWLITLEYELRLKPEGEWETIFVQ 390

QY 291 ET-YTLKTTNETRQLCFVVRKVNYSDD--GINSWSDKQCWE-GEDLSKKTLLRFLW 346
Db 391 QTOYKMFSLNPGKKYI-----IQHCKPDHGHGSWSENSENYIQIPNDFRVKDMI-VMI 443

QY 347 PFGFTLILVIFV 358
Db 444 VLGVLSLLICLI 455

RESULT 6
IL5R_MOUSE
ID IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).
GN IL5RA OR IL5R.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA Takatsu K.;
RT "Molecular cloning and expression of the murine interleukin-5
receptor";
RL EMBO J. 9:4367-4374(1990).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC ON B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90205; BAA14231.1; -
DR PIR: S12357; S12357.
DR MGI: MGI:96558; IL5ra.
DR InterPro: IPR000950; -
DR InterPro: IPR002465; -
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415
FT DOMAIN 18 339
FT TRANSMEM 340 361
FT DOMAIN 362 415
FT DISULFID 131 152
FT DISULFID 179 193
FT CARBOHYD 32 32
FT CARBOHYD 128 128
FT CARBOHYD 213 213
FT CARBOHYD 241 241
SQ SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 11.7%; Score 241; DB 1; Length 415;
Best Local Similarity 24.9%; Pred. No. 1.7e-12;
Matches 88; Conservative 65; Mismatches 144; Indels 56; Gaps 17;

QY 34 PPQDFEIVDPGYLYLQWQPLSLDHFKECTVEYELKYRNIGSEWTKITIKNLHKYD 93
Db 29 PPNVETIKATG-LAQVLLHWDPNPQEQ-RHVDLEVHVKINAPQEDYDTRKTES---KC 83

QY 94 GFDLNGKEAKIHTLLPWOCTNGSEVQSSWAEITWISQIPETKVQDMDCVYN---- 149
Db 84 VTPLEHGFSAASVRTILK---SSHTTTLASSWSAEI-KAPPGSPGTSVNTLCTTHTVSS 139

QY 150 -----WQY-LILCSWKPGIGVLLDTNNFLFYWYEGDHALQCVDYIK-ADGONICRPP- 200
Db 140 HTHLRPYQVSLRCTLWLVGKDAPEDQYFLYRFGVLTE--KQEYSRDLNRTACWFR 197

QY 201 -YLEASDYKDFYICVNGSENKPIRSSYFTFQLOQNIKVPPLPVYLTFTRESSEIKLWS 259
Db 198 TFINSKGFQELAVHINGSKRAAIKPPQDLFSPLADQVNPNNVTEESN-SLYIQWE 256

QY 260 IPLGPIPARCFDYEIEIRDD-----TTLVATVENETVTLKTTNETRQLCFVW 308
Db 257 KPLSAFPDCHCFNYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSIQ-----V 305

RA Willard H., Henthorn P.S.;
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
 in X-linked severe combined immunodeficiency, SCIDX1.";
 RL Hum. Mol. Genet. 2:1099-1104(1993).
 RN [4]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090315; PubMed-8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 RA Arai K.-I., Sugamura K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 RT receptors for IL-2 and IL-4.";
 RL Science 262:1874-1877(1993).
 RN [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090317; PubMed-8266078;
 RA Russell S.M., Kkegan A.D., Harada N., Nakamura Y., Noguuchi M.,
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-4 receptor.";
 RL Science 262:1880-1883(1993).
 RN [6]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE-94090316; PubMed-8266077;
 RA Noguuchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-7 receptor.";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE-95111955; PubMed-7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling.";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE-94130370; PubMed-8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding.";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANTS XSCID LYS-68.
 RX MEDLINE-94375038; PubMed-8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCIDX1 that
 RT differently affect the mRNA processing.";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANTS XSCID HIS-162.
 RX MEDLINE-94300093; PubMed-8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency.";
 RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANTS XSCID ASN-39.
 RX MEDLINE-95023932; PubMed-7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]

RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE-95397841; PubMed-7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency.";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANTS XSCID SER-183.
 RX MEDLINE-96013903; PubMed-7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Levinsky R.L., Kinnon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis.";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANTS XSCID GLN-237 G-H-W INS.
 RX MEDLINE-95164726; PubMed-7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma-chain mutation causing X-linked severe combined
 RT immunodeficiency.";
 RL J. Clin. Invest. 95:895-899(1995).
 RN [15]
 RP VARIANTS XSCID GLN-271.
 RX MEDLINE-95190013; PubMed-7883965;
 RA Schmalstieg F.C., Leonard W.J., Noguuchi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 RT moderate form of X-linked combined immunodeficiency.";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANTS XSCID ARG-115.
 RX MEDLINE-97042245; PubMed-8900089;
 RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B., Fischer A.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells.";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANTS XSCID GLN-285.
 RX MEDLINE-97295088; PubMed-9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinnon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation.";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANTS XSCID CYS-222.
 RX MEDLINE-98064061; PubMed-9399950;
 RA Sharfe N., Shahar M., Roifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology.";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 INTERLEUKINS.
 CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMGLOBULINEMIA, SWISS TYPE
 OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -!- DATABASE: NAME-PROW; NOTE-CD guide C0132 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".
 CC -!- DATABASE: NAME-IL2RGbase; NOTE-X-linked SCID mutation database;
 CC WWW="http://www.nhgri.nih.gov/DIR/GMBS/SCID/".
 CC -----
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RESULT 10
CYRG_MOUSE
ID CYRG_MOUSE STANDARD; PRT; 369 AA.
AC P34502;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors.";
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CBA/CA;
RC MEDLINE=93391374; PubMed=8378320;
RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RT IL-2R gamma chain expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma.";
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT chromosomal localization and expression in the adult thymus.";
RL Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=B6.S;
RX MEDLINE=96341745; PubMed=8750189;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44.";
RL J. Neuroconcol. 26:231-239(1995).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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DR EMBL; D13821; BAA02974.1; -
DR EMBL; U21795; AAA64279.1; -
DR EMBL; D13565; BAA02760.1; -
DR EMBL; L20048; AAA39286.1; -
DR EMBL; S75852; AAB32904.1; -
DR EMBL; S75844; AAB32904.1; JOINED.
DR EMBL; S75845; AAB32904.1; JOINED.
DR EMBL; S75847; AAB32904.1; JOINED.
DR EMBL; S75848; AAB32904.1; JOINED.
DR EMBL; S75849; AAB32904.1; JOINED.
DR EMBL; S75850; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR EMBL; S75337; CAA53085.1; -
DR PIR; JN0592; JN0592.
DR PIR; JN0775; JN0775.
DR MGD; MGI:96551; IL2rg.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 369
FT DOMAIN 23 263
FT TRANSMEM 264 284
FT DOMAIN 285 369
FT DOMAIN 151 250
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 71 71
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 96 96
FT CARBOHYD 159 159
FT CARBOHYD 164 164
SQ SEQUENCE 369 AA; 42241 MW; CB2D5AB459077AC7 CRC64;

Query Match 10.3%; Score 212.5; DB 1; Length 369;
Best Local Similarity 26.9%; Pred. No. 3,le-10;
Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKVDQDCVYNNQYLLCSN----KPGIGVLDDNYNLFYWEGLDHAL--QCVDYIK 189
DB 53 PFLPLVEVCFVFNIEMNCTWNSSEPQA-----TNLHLRYKVSDDNTFOECSHYLF 107

QY 190 ADQNGIGCRFPYLEASDYKDFYICVNGSSSEKPIRSSYFTFQIQNIVKPLPPVYLTFTRE 249
DB 108 SKEITSGCOIQKEDIQYTFVVL--QDPQKQRAVOKLNLQNLVPRAPENLTLSNL 165

QY 250 SSETIKLWSIPLGPIPARCFDYEIREDD--DTTLVATVENE--TYTLKTNETROLQCFV 307
DB 166 SESQLELRWK--SRHIKERCLQVLYQRNDRSWTELVNHEPRLSPVDELKRYTER 223

QY 308 VRSKYNIVCSDDGISENSDKOCWEG----EDLSKKTLLRFLWLPFGF--ILLIVIVTGL 361
DB 224 VRSRYNPIGSSQSKWSQPVHMGSHTVENPNSLFAELVLPVGTMLGLITLIFVCW 283

QY 362 LLRKNTVP 370
DB 284 LERMPPIPP 292

RESULT 11
CYRG_CANFA
ID CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
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Query Match 9.5%; Score 195; DB 1; Length 878;
Best Local Similarity 24.1%; Pred. No. 2.4e-08;
Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

QY 34 PPQDEIVDPGYLYLOWQPPPL---SLDHFKECTVEYELAKYRIGSTWTKITKLNH 90
DB 139 PKDHIHSPG---DHFLLEWSVSLGDSQVSWLSKDIEFVAYKRL-QDSWED--ASSLH 193
QY 91 YKDGFDLNGKIEAKTHTLPL-----WQCTNGSEQV---SSWAETTYWTSPOGIPET 138
DB 194 -TSNQVN--LEPKL--FLPNSIYARVTRLSAGSSLSGRPSRSPVHWDSQPG-DKA 247
QY 139 KYDDMDCVYNNQYLICSWKPKGIVLLDYNFLFYWGLDHALQCVDIKADGONI--- 195
DB 248 QPQNLCQFDDGIOSLCSWVWVTTQTSVSGFLYRPSAPAEKCSPPVVKPQASVYTR 307
QY 196 -CRRPYLEADYKDFYICVNGSSSENKPIRSSYFTFQONIVKPLPPVY-LFTTRESCE 253
DB 308 YRCSLPVPPEPSAHSQYTSVRHLEQCKFT-MSYHIQME-----PPILNQTKNRDS--- 357
QY 254 IKLWSIPLGPIPARCFD--YEIEIREDDTLVTATVEN---EYTLKTTNETRQLCFV 307
DB 358 YSLHETQKIP--KYIDHTFQVQKKSESWKDSTENLGRVNSMDLPQLPDPDTSYCAR 414
QY 308 VRSK-VNIYCSDDGIWSEWSDKQWEGEDLSKKTLLRFLWLPFGFILLIVFVFTGLLL 363
DB 415 VRVKPISDY---DGIWSEWSNEYTWT-TDWMVPTL---WI-----VLIIVFLIFTLL 460

RESULT 13
CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96268473; PubMed=8672241;
RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
gamma gene."
RL DNA Cell Biol. 15:453-459(1996).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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DB EMBL; U33748; AAB07812.1; -.
DB HSSP; P31785; 1ILN.
DB InterPro; IPR000950; -.
DB InterPro; IPR001777; -.
DB InterPro; IPR002465; -.

DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290 POTENTIAL.
FT DOMAIN 291 379 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 158 256 FIBRONECTIN TYPE-III.
FT DISULFID 68 78 POTENTIAL.
FT DISULFID 109 122 POTENTIAL.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.2%; Score 189.5; DB 1; Length 379;
Best Local Similarity 26.2%; Pred. No. 2.5e-08;
Matches 62; Conservative 42; Mismatches 106; Indels 27; Gaps 9;

QY 135 IPETKQDMDCVYNNQYLLCSW-----KPGIGVLLDYNFLFYWY---EGLDHALQCV 185
DB 61 LPLPKVQ---CFVFNVEYMNCTWNSSEPQ-----NNLTLYGYRNFNGDDKLQEGC 110
QY 186 DYKADGQNICRFPYLEADYKDFYICVNGSSSENKPIRSSYFTFQONIVKPLPPVILT 245
DB 111 HYLFGSEITSGCWGKKEIRLYETFVQIQDPREHR--KOPKOMLKLQDLQVWPAPENIT 168
QY 246 FTRESCEIKLWSIPLGPIPARCFDYEIEIREDDTLVTATVEN-EYTLKTTNETRQ 303
DB 169 LNLSEFQLELWS---NRYLDCHLEHLVQYRSDRDSRWTEQSDVDRHSFSLPSVDAQKL 225
QY 304 LCFVVRKVNIIYCSDDGIWSEWSDKQWEGEDLSKKTLLRFLWLPFGFILLIVFVFTG 360
DB 226 YTFVRVRSRYNPLCGSAQHWSDMSYPIHW-GSNTSKENIENPENPSLFALEAVLPLG 281

RESULT 14
CYRG_HUMAN
ID CYRG_HUMAN STANDARD; PRT; 897 AA.
AC P32927;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR (CDW131 ANTIGEN).
GN CSF2RB OR IL5RB OR IL3RB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9108571; PubMed=1702217;
RA Hayashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
RA Miyajima A.;
RT "Molecular cloning of a second subunit of the receptor for human
granulocyte-macrophage colony-stimulating factor (GM-CSF):
reconstitution of a high-affinity GM-CSF receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
RN [2]
RP REVISION TO 454.
RA Kitamura T.;
RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw131 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw131.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M59941; AAA18171.1; -
CC PIR: A39255; A39255.
CC MIM: 138981; -
CC InterPro: IPR000950; -
CC InterPro: IPR001777; -
CC InterPro: IPR002465; -
CC Pfam: PF00041; fn3; 2.
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 897 CYTOKINE RECEPTOR COMMON BETA CHAIN.
FT DOMAIN 17 443 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 444 460 POTENTIAL.
FT DOMAIN 461 897 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 129 238 FIBRONECTIN TYPE-III.
FT DOMAIN 336 434 FIBRONECTIN TYPE-III.
FT DISULFID 35 45 BY SIMILARITY.
FT DISULFID 75 91 BY SIMILARITY.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 897 AA; 97335 MW; 339837FDB8F393A CRC64;

Query Match 8.7%; Score 178.5; DB 1; Length 897;
Best Local Similarity 22.5%; Pred. No. 5.6e-07;
Matches 89; Conservative 57; Mismatches 144; Indels 105; Gaps 21;

QY 32 VNPQDFEIVDPGYLGY-----LYLQWQPP-----LSLDHF----- 62
DB 97 VPCQSFVVDVDFSPQDRPLGLRLVTLLQHVQPPPEPRDLQISTDODHLLTWSVAL 156

QY 63 -----KECTVEYELKYNIGSETK--TIITKNLHYKDGFDLNKIGIE-----A 103
DB 157 GSPQSHWLSPGDLEFVYVKRL-QDSWEDAAILLNTS-----QATLGPHEHLMPSITYVA 210

QY 104 KIHT-LLPWQCTNGSEVQSSWAETTYWISPGIPETKVDMDCVYNNQYLLCSWKPGIG 162
DB 211 RVTRTLAGPSRLSGR--PSKWSPEVCWDSQPG-DEAQPNLECFDFDGAAVLSCSWEVRKE 267

QY 163 VLLDNTNLYFWYEGLDHALQCVYIKADGONIG-----CRFPYLEASDYKDFYICVN 215
DB 268 VASSVFGFLYKPSDAGEECSPLVR---EGLSLHTRHHQCIQVPPQATHGQIVSVQ 324

QY 216 GSSENKPIRSYFTFQLQINIVPLPPVLTFTRESSCEIKLKWISPLGPPIPARCFDYETE 275
DB 325 PRRAEKHKISSV-----NI--QMAPPSLNTVKDGD-SYSLRWETMKMYEHIDHTFEIQ 375

QY 276 IREDDTTLVAT-VENETVLTATN-----ETRLQCFV-VRSKNVIYCDSDGIVSE 324
DB 376 YRKD-----TATWKDSKTELTQNAHSMALPALESTRYKWARVRVTRTSGY---NGIWE 427

QY 325 WSDKOCWEGEDLSKTLRLLPFGFILLVLFVT 359
DB 428 WSEARSWTESV-----LPMWVLIVILFT 453

RESULT 15
CYRB_MOUSE
ID CYRB_MOUSE STANDARD; PRT; 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR.
GN CSF2RB OR CSF2B1 OR AIC2B OR IL3RB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90319131; PubMed-1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M34397; AAA37204.1; -
CC PIR: A35782; A35782.
CC MGD: MGI:1339759; Csf2rb1.
CC InterPro: IPR000950; -
CC InterPro: IPR001777; -
CC InterPro: IPR002465; -
CC Pfam: PF00041; fn3; 2.
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 896 CYTOKINE RECEPTOR COMMON BETA CHAIN.
FT DOMAIN 23 441 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 442 463 POTENTIAL.
FT DOMAIN 464 896 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 132 241 FIBRONECTIN TYPE-III.
FT DOMAIN 343 440 FIBRONECTIN TYPE-III.
FT DISULFID 39 49 BY SIMILARITY.
FT DISULFID 77 94 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 896 AA; 99111 MW; 8CE16EDFDC07A999 CRC64;

Query Match 8.4%; Score 173.5; DB 1; Length 896;
Best Local Similarity 20.7%; Pred. No. 1.4e-06;
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

QY 5 CIAIGCLTFLISTITFTGCTS-----SSDTEIK-----VNPQDFEIVDPGYLGY 48
DB 94 CVPRCVIPY---TFESITNEDYYSFRPDSDLGIQLMPLAQNVQPPLPKNVISISSEDR 150

QY 49 LYLQWQPP-----SLDHFKECTVEYELKYNIGSETFWTKITKN-----LHYKDGFDLNKG 100
DB 151 FLEMSVSLGDAQVSWLSSKDIETFEVAYKRL-QDSWEDAYSLSHTSKFQVNFEPKLFLENS 209

QY 101 IEA-KIHT-LLPWQCTNGSEVQSSWAETTYWISPGIPETKVDMDCVYNNQYLLCSWK 158
DB 210 IYAPRVTRTLYPGSSLSGR--PSRWSPRAHWDSQPG-DKAQPNLQCFDFDGIQSLSWNE 266

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:03 ; Search time 60.7 Seconds
(without alignments)
371.534 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372

Perfect score: 2056

Sequence: 1 MAFVCAIGCLYFLISTTF.....ILVIFVTGLLRKPNTPYK 372

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 2056 | 100.0 | 380 | AAW24972 | Human interleukin- |
| 2 | 2056 | 100.0 | 380 | AAW35295 | Human IL-13 bindin |
| 3 | 2056 | 100.0 | 380 | AAW36613 | Human Zcytor2 cyto |
| 4 | 2056 | 100.0 | 380 | AAW41520 | Human HR-1 recepto |
| 5 | 2056 | 100.0 | 380 | AAW41502 | Human cytokine/pep |
| 6 | 2056 | 100.0 | 380 | AAW33603 | Homo sapiens HR-1 |
| 7 | 2056 | 100.0 | 380 | AAW35296 | IL-13 binding chai |
| 8 | 2056 | 100.0 | 380 | AAW72136 | Human interleukin |
| 9 | 2056 | 100.0 | 380 | AAW29748 | Human IL-13 recept |
| 10 | 2030 | 98.7 | 380 | AAW36614 | Human Zcytor2 cyto |
| 11 | 1853 | 90.1 | 372 | AAW36616 | Celebus macaque Zc |

| | | | | | | |
|----|--------|------|------|----|----------|--------------------|
| 12 | 1753 | 85.3 | 315 | 19 | AAW56261 | Mature interleukin |
| 13 | 1753 | 85.3 | 359 | 19 | AAW56260 | Construct containi |
| 14 | 1194.5 | 58.1 | 383 | 18 | AAW35294 | Murine IL-13 bindi |
| 15 | 1194.5 | 58.1 | 383 | 21 | AAW95295 | IL-13 binding chai |
| 16 | 1194.5 | 58.1 | 383 | 22 | AAW72135 | Murine interleukin |
| 17 | 1194.5 | 58.1 | 383 | 22 | AAW29747 | Mouse IL-13 recept |
| 18 | 456 | 22.2 | 157 | 19 | AAW56252 | Interleukin-13 bin |
| 19 | 310.5 | 15.1 | 396 | 13 | AAW22216 | Sequence of human |
| 20 | 310.5 | 15.1 | 396 | 13 | AAW22220 | Sequence of secret |
| 21 | 310.5 | 15.1 | 420 | 13 | AAW22219 | Human interleukin- |
| 22 | 310.5 | 15.1 | 420 | 19 | AAW82842 | Sequence of secret |
| 23 | 309.5 | 15.1 | 421 | 13 | AAW25064 | Human IL-5 recepto |
| 24 | 304.5 | 14.8 | 420 | 13 | AAW22215 | Sequence of human |
| 25 | 297 | 14.4 | 313 | 18 | AAW21856 | Protein used in pr |
| 26 | 294.5 | 14.3 | 427 | 18 | AAW24973 | Human interleukin- |
| 27 | 294.5 | 14.3 | 427 | 22 | AAW19807 | Human interleukin- |
| 28 | 293.5 | 14.3 | 426 | 18 | AAW09822 | Human interleukin- |
| 29 | 292.5 | 14.2 | 426 | 18 | AAW09821 | Mouse interleukin- |
| 30 | 292.5 | 14.2 | 1026 | 16 | AAW70121 | IL5-R-GBP 130 fusi |
| 31 | 292 | 14.2 | 335 | 13 | AAW25063 | Soluble human IL-5 |
| 32 | 292 | 14.2 | 335 | 14 | AAW33699 | shIL-5R-alpha. Sy |
| 33 | 285.5 | 13.9 | 427 | 22 | AAW19808 | Human interleukin- |
| 34 | 285 | 13.9 | 793 | 21 | AAW92208 | IL-13/IL-4 dual tr |
| 35 | 284 | 13.8 | 784 | 21 | AAW92207 | IL-13/IL-4 dual tr |
| 36 | 242 | 11.8 | 398 | 13 | AAW22212 | Sequence of interl |
| 37 | 241 | 11.7 | 415 | 13 | AAW22211 | Sequence of interl |
| 38 | 241 | 11.7 | 415 | 13 | AAW22217 | Sequence of interl |
| 39 | 229 | 11.1 | 315 | 13 | AAW22214 | Sequence of interl |
| 40 | 229 | 11.1 | 332 | 13 | AAW22213 | Sequence of interl |
| 41 | 229 | 11.1 | 332 | 13 | AAW22218 | Sequence of interl |
| 42 | 220 | 10.7 | 369 | 15 | AAW47148 | IL-2 receptor gamm |
| 43 | 219 | 10.7 | 347 | 15 | AAW47149 | IL-2 receptor gamm |
| 44 | 209.5 | 10.2 | 369 | 15 | AAW59094 | Murine IL-2R gamma |
| 45 | 209 | 10.2 | 482 | 19 | AAW31646 | Human cytokine rec |

ALIGNMENTS

RESULT 1
AAW24972
ID AAW24972 standard; protein; 380 AA.
AC AAW24972;
DT 22-JUN-1998 (first entry)
XX Human interleukin-13 beta receptor.
DE Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
KW Homo sapiens.
XX OS
XX PN W03720926-A1.
XX PD 12-JUN-1997.
XX PF 07-NOV-1996; 96WO-FR01756.
XX PR 06-DEC-1995; 95FR-0014424.
XX PA (SNFI) SANOFI SA.
XX PI Caput D, Ferrara P, Laurent P, Vita N;
XX DR WPI; 1997-319773/29.
XX DR N-PSDB; AAT85826, AAT86464.
XX PT New purified human interleukin-13 receptors - and related nucleic
XX PT acids, useful for diagnosis and treatment of inflammation, allergy,
XX PS Claim 1; Figure 2a; 83pp; French.

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are designated IL-13R beta and alpha respectively.
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunoassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFISTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
 DB 1 mafvclaigclytlfstfgctssdteikvnpqdfeidvpgylglylqwpplslid 60

QY 61 HFKECTVEYELKYRIGSETWKTITKNLHYKDGFDLNGKIEAKHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkyrnigsetwktitknlhykdgfdlnkgleakhtllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGLVLDNTNLYFWYEGLDH 180
 DB 121 sswaettywispgipetkvqdmcdvynnyqyllcswkpglgvldntnlyfwyegldh 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQNLQIVKPLP 240
 DB 181 alqcvdyikadqngicrcfpyleasdykdfyicvngsssenkpirssyftfqnlqivkplp 240

QY 241 PYYLFTRESSCEIKLWSIPGPAPRCFDEYIEIREDDTLVTATVENETYLTKTNE 300
 DB 241 ppylftressceiklwsipgiparcfdyeyieireddtlvtatvenetylktne 300

QY 301 TRQLCFVVRKSNVNIYCSDDGIWSEWSKOCWEGEDLSKTKTLRLFWLPFGFILLVIFVTG 360
 DB 301 trqlcfvvrksnvniycsddgiwsewsdkocwgedlskktlrlfwlpfgflllvifvtg 360

QY 361 LLLRRKNTYPKM 372
 DB 361 lllrkntypkm 372

RESULT 2

AAW35295
 ID AAW35295 standard; Protein: 380 AA.

XX
 AC AAW35295;

XX
 DT 27-MAR-1998 (first entry)

XX
 DE Human IL-13 binding chain of the IL-13 receptor.

XX
 KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.

XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= signal_sequence
 FT /note= "putative"
 FT Protein 26..380
 FT /label= mature_protein
 FT Domain 26..341
 FT /label= extracellular_domain
 FT Domain 342..362
 FT /label= transmembrane_domain
 FT Domain 363..380
 FT /label= intracellular_domain

XX WO9731946-A1.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-US03124.

XX 01-MAR-1996; 96US-0609572.

XX (GEMY) GENETICS INST INC.

XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;

XX WPI; 1997-448632/41.

XX N-PSDB; AAT95214.

XX New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis

XX Claim 11; Pages 34-35; 49pp; English.

XX The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.

XX Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFISTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60

DB 1 mafvclaigclytlfstfgctssdteikvnpqdfeidvpgylglylqwpplslid 60

QY 61 HFKECTVEYELKYRIGSETWKTITKNLHYKDGFDLNGKIEAKHTLLPWQCTNGSEVQ 120

DB 61 hfkectveyelkyrnigsetwktitknlhykdgfdlnkgleakhtllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGLVLDNTNLYFWYEGLDH 180

DB 121 sswaettywispgipetkvqdmcdvynnyqyllcswkpglgvldntnlyfwyegldh 180

QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240
Db 181 alqcvdyikadqngicrpfyleasdykdfyicvngsenkpirssyftfqlqniakplp 240
QY 241 PVLFTRESSCEIKLWSIPLGPAPRCFDEYIEIREDDTLVATVENETYLKTTNE 300
Db 241 pvlftressceiklwsiplgpparcfdyeieireddtlvtatvenetytlktne 300
QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGDLKSKTLIRFWLPRGFILILVIFVTG 360
Db 301 trqlcfvvrsvniycsddgiwsewsdkqcegedlskttlirfwlprgfllilvifvtg 360
QY 361 LLLRKPNTYPKM 372
Db 361 llrrkpntypkm 372

RESULT 3

AAW36613
ID AAW36613 standard; Protein: 380 AA.

AC AAW36613;

DT 30-MAR-1998 (first-entry)

DE Human zcytor2 cytokine receptor protein.

KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Domain 340..363
FT /label= transmembrane_domain
FT Domain 364..380
FT /label= intracellular_domain
FT Domain 25..339
FT /label= ligand_binding_domain

PN WO9733913-A1.

XX 18-SEP-1997.

PD 12-MAR-1997; 97WO-US04043.

PR 13-MAR-1996; 96US-0013345.

XX (ZYMO) ZYMOGENETICS INC.

XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'Hara PJ;

XX WPI; 1997-470820/43.
DR N-PSDB; AAT96782.

XX New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment

XX Claim 2; Page 47-48; 79pp; English.

XX This sequence represents a novel ligand-binding receptor, zcytor2,
CC which shares homology with cytokine receptors and was isolated from human
CC placental polyA+ RNA. The resulting polypeptide is a receptor for
CC cytokines (particularly interleukin-13) and is expressed on the surface
CC of testicular cells, probably being involved in spermatogenesis. It can
CC be used to detect ligands that promote proliferation and/or
CC differentiation of such cells in cultures and may also be used to treat
CC infertility. Antagonists of this receptor may be used to characterise
CC ligand-receptor interactions and as male-specific contraceptives. By
CC blocking the action of IL-13, receptor antagonists and ligand-binding
CC this receptor can also be used to modulate immune function, e.g. in

CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.

XX Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 18; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTFLLISTTGTCTSSDTEIKVNPQQDFEIVDPGVLGYLYLQWOPPLSLD 60
Db 1 mafvclaigclytfllisttgtctssdteikvnpqqdfeidvpgylglylqwpplslid 60

QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLKNKIEAKIHTLLPQCTNGSEVQ 120
Db 61 hfkectveyelkyrnigsetwktitknhykgdgdlnkgleakihltlpwqctngsevq 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYVWQYLLCSWKPGICVLLDTNLYWYEGLDH 180
Db 121 sswaettywispgipetkvqdmcdvyywnqyylcswkpgigvlltdtnlyfwyegldh 180

QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240
Db 181 alqcvdyikadqngicrpfyleasdykdfyicvngsenkpirssyftfqlqniakplp 240

QY 241 PVLFTRESSCEIKLWSIPLGPAPRCFDEYIEIREDDTLVATVENETYLKTTNE 300
Db 241 pvlftressceiklwsiplgpparcfdyeieireddtlvtatvenetytlktne 300

QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGDLKSKTLIRFWLPRGFILILVIFVTG 360
Db 301 trqlcfvvrsvniycsddgiwsewsdkqcegedlskttlirfwlprgfllilvifvtg 360

QY 361 LLLRKPNTYPKM 372
Db 361 llrrkpntypkm 372

RESULT 4

AAW41520
ID AAW41520 standard; Protein: 380 AA.

AC AAW41520;

DT 22-JUN-1998 (first entry)

DE Human HR-1 receptor.

XX HR-1 receptor; human; cytokine; infection; asthma; allergy;
KW haematopoietic disorder; tumour; therapy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Sig_peptide
FT Protein 22..380
FT /label= Mat_protein

XX WO9747741-A1.

XX 18-DEC-1997.

XX 12-JUN-1996; 96WO-US10262.

XX 12-JUN-1996; 96WO-US10262.

XX (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Appelbaum ER, Hu J;
 XX WPI: 1998-052308/05.
 DR N-PSDB; AAV04131.
 XX
 XX Nucleic acid sequence encoding human cytokine peptide hormone
 PT receptor - useful to treat, prevent or diagnose, e.g. lowered
 PT resistance to infection, asthma, allergy or haematopoietic disease
 XX
 PS Claim 13; Page 62-64; 76pp; English.
 XX
 CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated the HR-1 receptor, that shows 27% identity
 CC and 52% similarity to the interleukin-5 receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
 CC human testis library. Recombinant HR-1 receptor can be expressed
 CC in claimed host cells, and used in a claimed method for identifying
 CC compounds which bind to, and activate or inhibit, it. HR-1
 CC receptor activators and agonists can be used to treat, prevent or
 CC diagnose predisposition to lowered resistance to infection, asthma,
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
 CC be used to treat conditions associated with HR-1 receptor
 CC overexpression. The antibodies can also be used to determine HR-1
 CC receptor levels, since overexpression may be diagnostic of tumours.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTISTFGCTSSDTEIKVNPDPDFEIVDPGYLGVLQWQPPLSLD 60
 Db 1 mafvclaigcltyflistftgctssdteikvnpdpdfeivdpgylgylylqwqpplslid 60

QY 61 HFKECTVEYELKYNIGSETWKTITKLNHYKDGFDLNGKIEAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlhykdgfdlnkgeakhtllpwqctngsevg 120

QY 121 SSWAETTWISPOGIPETKVDMDCVYNNWQYLLCSWKPGLVLDTNVNFYWEGLDH 180
 Db 121 sswaettwispgipetkvdmdcvyynnwqyllcswkpglvgldtnvnfywvegl dh 180

QY 181 ALQCDVYKADGQNGICRPPYLEADYKDFYTCVNGSSENKPIRSSYTFQQLNIVKPLP 240
 Db 181 alqcdvyikadgngicrpfyleadykdfytcvngssenkprrssytfqqlnivkplp 240

QY 241 PVLFTRESSCEIKLWSIPLGPAPARCFDYIEIREDDTLVATVENETYLTKTNE 300
 Db 241 pvlftressceiklwsiplgpparcfdyieireddtlvatvenetylktktne 300

QY 301 TROLCFVRSKNVNYICSDGIIWSESDKQWGEDLSKTKLLRFLWLPFGFIIILVIFVTG 360
 Db 301 trqlcfvrsknvnyicsdgiwsewskqwedlsktkllrflwlpfgfiiilvifvtg 360

QY 361 LLLRPNYIPKM 372
 Db 361 lllrpnypkm 372

RESULT 5
 AA41502
 ID AA41502 standard; Protein: 380 AA.
 XX
 AC AA41502;
 XX
 DT 08-JUN-1998 (first entry)
 XX Human cytokine/peptide receptor, HR-1 receptor.

XX HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
 KW neutropenia; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT 22..380
 FT Protein
 FT /label= Mat_protein
 FT /note= "Claim 14"
 XX
 XX EP812913-A2.
 XX 17-DEC-1997.
 XX 04-JUN-1997; 97EP-0303815.
 XX 12-JUN-1996; 96US-0017843.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Appelbaum ER, Hu J;
 XX WPI: 1998-034974/04.
 DR N-PSDB; AAV04075.
 XX
 XX Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 XX
 PS Claim 13; Page 27-28; 34pp; English.
 XX
 CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor. The amino acid sequence
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human
 CC testis cDNA library. It shows 27% amino acid identity and 52%
 CC similarity with the human interleukin-5 receptor. Also claimed are
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an
 CC agonist to the polypeptide, antibody against the polypeptide, an
 CC antagonist that inhibits the activity of the polypeptide, a process
 CC for diagnosing a disease, or a susceptibility to disease, related
 CC to expression of HR-1 receptor, and a method for identifying
 CC compounds that activate or inhibit the HR-1 receptor. HR-1
 CC receptor protein and polynucleotides can be used for research,
 CC biological, diagnosis and (gene) therapy applications, e.g. to
 CC increase resistance to infections in individuals with trauma and/or
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTISTFGCTSSDTEIKVNPDPDFEIVDPGYLGVLQWQPPLSLD 60
 Db 1 mafvclaigcltyflistftgctssdteikvnpdpdfeivdpgylgylylqwqpplslid 60

QY 61 HFKECTVEYELKYNIGSETWKTITKLNHYKDGFDLNGKIEAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlhykdgfdlnkgeakhtllpwqctngsevg 120

QY 121 SSWAETTWISPOGIPETKVDMDCVYNNWQYLLCSWKPGLVLDTNVNFYWEGLDH 180
 Db 121 sswaettwispgipetkvdmdcvyynnwqyllcswkpglvgldtnvnfywvegl dh 180

Db 121 sswaettywispqgipetkvqmdcvyywnqyllcswkpgigvllidtnynlfwyegldh 180
QY 181 ALQCVDYIKADGQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLP 240
Db 181 alqcvdyikadgqntgcrfpyleasdykdfyicvngsssenkpirssyftfqiqlnvkplp 240
QY 241 PVLFTRESSCEIKLWSIPLGPIPARCFDYEIREDDDTLVATVENETYTLKTNE 300
Db 241 pvlftressceiklwsiplgpiparcfdyeiireddtlvtatvenetytlktne 300
QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGDELKTLRFLWLPFGFILLIVFVVG 360
Db 301 trqlcfvvrksvniycsddgiwsewsdkqcegedlskllrflwlpfgfllilvifvtg 360
QY 361 LLRRKPNTYPKM 372
Db 361 llrrkpntypkm 372
RESULT 6
AAW33603
ID AAW33603 standard; Protein; 380 AA.
XX
AC AAW33603;
DT 08-JUN-1998 (first entry)
XX
DE Homo sapiens HR-1 receptor.
XX
KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;
KW syndrome; aplastic anaemia; neutropenia; cancer treatment;
KW infection resistance; diagnosis; tumours; HR-1 receptor;
KW asthma; allergic; haematopoietic; disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
XX
PN WO9747742-A1.
XX
PD 18-DEC-1997.
XX
PF 09-JUL-1996; 96WO-US11459.
XX
PR 12-JUN-1996; 96WO-US10262.
PR 12-JUN-1996; 96US-0017843.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMK) SMITHKLINE BEECHAM CORP.
XX
PI Appelbaum ER, Hu J;
XX
DR WPI; 1998-052309/05.
DR N-PSDB; AAV02295.
XX
PT DNA encoding human cytokine-peptide hormone receptor - useful for
PT treating preventing or diagnosing, e.g. lowered resistance to
PT infection, asthma, allergy, or haematopoietic disease
XX
PS Claim 15; Fig 1; 75pp; English.
XX
CC The sequence is that of the human cytokine/peptide hormone receptor
CC (HR-1 receptor). This, or its activators or agonists, can be used to
CC treat, prevent or diagnose predisposition to lowered resistance to
CC infection, asthma, allergic or haematopoietic disorders, e.g. where
CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
CC neutropenia or cytotoxic treatments for cancer. Antagonists of the
CC receptor, e.g. antibodies or fragments of it may be used to treat
CC conditions associated with overexpression of the HR-1 receptor, e.g.
CC those listed above. Antibodies may also be used to assay levels of HR-1
CC receptor, overexpression of which may be diagnostic of tumours, by usual

CC immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
CC for affinity purification of the HR-1 receptor.
SQ Sequence 380 AA;
Query Match 100.0%; Score 2056; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYFTLIISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
Db 1 mafvclaigclyftliistftgctssdteikvnpqdfeidvpgylylqwpplslid 60
QY 61 HPEKCTVEYELKRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
Db 61 hpektveyelkrynigsetwktiitknlnhykdgfdlnkgleakihllpwqctngsevq 120
QY 121 SSWAETTYWISPGIPETKVQMDCVYYNWOYLLCSWKPGLVLLDTNLYNLFYWEGLDH 180
Db 121 sswaettywispqgipetkvqmdcvyywnqyllcswkpgigvllidtnynlfwyegldh 180
QY 181 ALQCVDYIKADGQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLP 240
Db 181 alqcvdyikadgqntgcrfpyleasdykdfyicvngsssenkpirssyftfqiqlnvkplp 240
QY 241 PVLFTRESSCEIKLWSIPLGPIPARCFDYEIREDDDTLVATVENETYTLKTNE 300
Db 241 pvlftressceiklwsiplgpiparcfdyeiireddtlvtatvenetytlktne 300
QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGDELKTLRFLWLPFGFILLIVFVVG 360
Db 301 trqlcfvvrksvniycsddgiwsewsdkqcegedlskllrflwlpfgfllilvifvtg 360
QY 361 LLRRKPNTYPKM 372
Db 361 llrrkpntypkm 372
RESULT 7
AAW95296
ID AAW95296 standard; Protein; 380 AA.
XX
AC AAW95296;
XX
DT 12-SEP-2000 (first entry)
XX
DE IL-13 binding chain of human IL-13 receptor.
XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"
FT Protein 26..380
FT /note= "mature protein"
FT Domain 26..341
FT /note= "extracellular domain; a polypeptide
FT comprising amino acids 22-334 is
FT specifically claimed in Claim 11(e)"
FT Domain 342..362
FT /note= "transmembrane domain"
FT Domain 363..380
FT /note= "intracellular domain; a polypeptide
FT comprising amino acids 257-383 is
FT specifically claimed in Claim 11(f)"
XX

PN WO200036103-A1.
XX 22-JUN-2000.
PD 13-DEC-1999; 99WO-US29493.
PF 14-DEC-1998; 98US-0211335.
XX (GEMY) GENETICS INST INC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;
XX WPI; 2000-431587/37.
DR N-PSDB; AAA27912.
XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
PT asthma, Grave's disease and inflammatory conditions of the lung -
XX Claim 11(d); Page 53-54; 60pp; English.
XX The present sequence is that of the interleukin-13 binding chain
CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
CC the haematopoietin receptor family that acts as a mediator of
CC IL-13. The invention provides methods for the recombinant
CC production of IL-13bc polypeptides, including claimed full-length
CC IL-13bc, its extracellular domain, and its intracellular domain.
CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
CC of IL-13 and its receptor) can be used to treat conditions in
CC which IL-13 is implicated, particularly IgE-mediated conditions and
CC diseases including atopy, allergy, asthma, immune complex diseases
CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
CC thyroiditis and Grave's disease), lung inflammation,
CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
CC activation, IL-13bc proteins can also be used to enhance macrophage
CC activation, e.g. in vaccination, treatment of mycobacterial or
CC intracellular organisms or parasite infections. IL-13bc proteins
CC may also be used to potentiate the effects of IL-13 in vitro and
CC in vivo, as diagnostic agents, and to screen for agents capable of
CC binding to IL-13bc or IL-13 receptor, or which interfere with the
CC binding of IL-13 to its receptor.
XX Sequence 380 AA;
SQ

Query Match 100.0%; Score 2056; DB 21; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLYTLFTSTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPLSLD 60
Db 1 mafvclatgcltytlftstgctssdteikvnpqdfeidvdpgylylqwpplslid 60
QY 61 HFKECTVEYELKYRNIGSETWKTITLTKNLHYKDGFDLANKGLEAKIHTLLPWQCTNGSEVQ 120
Db 61 hfkectveyelkyrnigsetwktitltnlhykdgfdlnkgleakhtllpwqctngsevq 120
QY 121 SSWAETTYWISPGQIPETKVQDMDCVYVNWQYLLCSWRKPGIGVLDTNINLFYWYEGLDH 180
Db 121 sswaettywispgqipetkvqdmdevynwqyllcswrkpgigvlltdtnynlfywyegldh 180
QY 181 ALQCVDYIKADQNGICGRFPYLEASDYKDFICVNGSSSENKPIRSSYTFQIQNVKPLP 240
Db 181 alqcvdyikadqngicgrfpyleasdykdfyicvngsssenkpirssytfqlqnvkplp 240
QY 241 PVIYFTRESSCEIKKWSIPLGPAPCFDYIEIREDDTTLVTATVENETYLTKTNE 300
Db 241 pviyftressceikkwsiplgpaprcfdyieireddttlvtatvenetyltktnne 300

QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSDKQCEGDLSSKTLRFLWLPFGFILLIVFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewdskqcegedlskttlrlfwlpfgfillivfvtg 360
QY 361 LLRLKPNTPYPMK 372
Db 361 llrlkpnptypkm 372
RESULT 8
AAAY72136
ID AAY72136 standard; Protein; 380 AA.
XX
AC AAY72136;
XX
DT 24-APR-2001 (first entry)
XX
DE Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
XX Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
XX therapy; tissue fibrosis; Schistosoma infection; surgical incision;
KW cytostatic; wound; IL-13 related condition; allergic condition;
KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
KW macrophage activation.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..25 /label= Signal_peptide
FT Region 1..81 /note= "This region is identical to the translated
FT sequence of an expressed sequence tag (EST) identified
FT as y999f10.rl human cDNA clone 41648 5"
FT Protein 26..380 /label= Mature_human_interleukin (IL)-13_binding_chain_
FT of_IL-13_receptor
FT Domain 26..341 /note= "Extracellular domain; this region is specifically
FT claimed in claims 1e, 6e, 15e and 23e"
FT Domain 342..362 /note= "Transmembrane domain"
FT Domain 363..380 /note= "Intracellular domain; this region is specifically
FT claimed in claims 1f, 6f, 15f and 23f"
XX
PN WO200078336-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-US17103.
XX
PR 21-JUN-1999; 99US-0334512.
XX (GEMY) GENETICS INST INC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;
XX WPI; 2001-080753/09.
DR N-PSDB; AAD02335.
XX
PT Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
PT in a mammalian subject, involves administering a pharmaceutical
XX composition comprising IL-13 antagonist -
PS Claim 1a; Page 69-70; 72pp; English.
XX The invention relates to a method of treating, or inhibiting
CC the formation of tissue fibrosis in mammals, which involves
CC administering a pharmaceutical composition comprising interleukin
CC (IL)-13 antagonist. The protein of the invention is useful for

CC treating tissue fibrosis resulting from infection with Schistosoma
 CC or from healing of a wound which is a surgical incision, or
 CC inhibiting formation of tissue fibrosis which affects tissues such
 CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 CC biliary tract and gut. It is also used in the treatment or modulation
 CC of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
 CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTFGCTSSDTEIKVNPQDPFEIVDPGVLGYLYLQWQPPSLD 60
 Db 1 mafvclaigcllytlstfgctssdteikvnpqdpfeivdpvglylylqwppslid 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITTKNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkyrnigsetwktitknlhykdgfdlnkgeakihltlpwqctngsevg 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNWOYLCSWKPGLGVLDNTNLYFYWYEGLDH 180
 Db 121 sswaettywispgqipetkvdmdcvynnwqylcswkpglgvldntnlyfywyegldh 180
 QY 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYTFQLONIKVPPLP 240
 Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkiprissytfqlqniavkplp 240
 QY 241 PVYLFTRESSCEIKLWSIPLGPAPCFDYEIRDDDTTLVTATVENETYLTKTNE 300
 Db 241 pvyllftressceiklwsiplgpiarpcfdyeirdddtlvtatvenetylktktne 300
 QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 Db 301 trqlcfvvrksvniycsddgiwsewsdkqcegedlskktllrflwlpfgfllilvifvtg 360
 QY 361 LLLRKPNTPYPM 372
 Db 361 lllrkpnitypkm 372

RESULT 9
 AAB29748
 ID AAB29748 standard; Protein; 380 AA.
 XX
 AC AAB29748;
 XX
 XX
 DT 23-FEB-2001 (first entry)
 XX
 DE Human IL-13 receptor IL-13 binding chain (IL-13bc).
 KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
 KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnery;
 KW wound healing; schistosoma infection; liver; skin; muscle;
 KW cartilage; cardiac tissue; lung tissue; uterine tissue;
 KW intestinal tissue; vascular tissue; neural tissue.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200064944-A1.
 XX
 PD 02-NOV-2000.
 XX

PF 28-APR-2000; 2000WO-US11612.
 XX
 PR 28-APR-1999; 99US-0301808.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
 PI Whitters MJ, Wood C;
 XX
 DR WPI; 2001-024676/03.
 DR N-PSDB; AAC81416.
 XX
 PT Treating or inhibiting tissue fibrosis resulting from infection with
 PT schistosoma and wound healing involves administering interleukin-13 or
 PT interleukin-4 antagonist
 XX
 XX Claim 1; Page 76-77; 82pp; English.

XX The invention relates to a method of treating fibrosis in a mammal
 CC by administering an interleukin-13 (IL-13) antagonist or an IL-4
 CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding
 CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or
 CC soluble fragments thereof. The method is useful for treating or
 CC inhibiting the formation of tissue fibrosis resulting from the healing
 CC of a wound, including a surgical incision wound, or from infection with
 CC schistosoma. The method may be used to treat fibrosis in a variety of
 CC tissues, particularly liver tissue, but also skin epidermis, skin
 CC endodermis, muscle, tendon, cartilage, cardiac tissue, pancreatic
 CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,
 CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
 CC tissue. The present sequence represents human IL-13bc.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTFGCTSSDTEIKVNPQDPFEIVDPGVLGYLYLQWQPPSLD 60
 Db 1 mafvclaigcllytlstfgctssdteikvnpqdpfeivdpvglylylqwppslid 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITTKNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkyrnigsetwktitknlhykdgfdlnkgeakihltlpwqctngsevg 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNWOYLCSWKPGLGVLDNTNLYFYWYEGLDH 180
 Db 121 sswaettywispgqipetkvdmdcvynnwqylcswkpglgvldntnlyfywyegldh 180
 QY 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYTFQLONIKVPPLP 240
 Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkiprissytfqlqniavkplp 240
 QY 241 PVYLFTRESSCEIKLWSIPLGPAPCFDYEIRDDDTTLVTATVENETYLTKTNE 300
 Db 241 pvyllftressceiklwsiplgpiarpcfdyeirdddtlvtatvenetylktktne 300
 QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 Db 301 trqlcfvvrksvniycsddgiwsewsdkqcegedlskktllrflwlpfgfllilvifvtg 360
 QY 361 LLLRKPNTPYPM 372
 Db 361 lllrkpnitypkm 372

RESULT 10
 AAW36614
 ID AAW36614 standard; Protein; 380 AA.
 XX
 AC AAW36614;

Query Match 90.1%; Score 1853; DB 18; Length 372;
Best Local Similarity 92.2%; Pred. No. 1.6e-172;
Matches 343; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLYFLISTFCTSSDSEIKVNPQDFEIVDPGVLGYLQWQPPSLD 60
DB 1 mafvylalrcictflistftgyststdeikvnpqdfiwdpgylgylylqwgppslid 60

QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLKNKTEAKHTLLPWQCTNGSEVQ 120
DB 61 nfkectveyelkynigsetwtiitknlhykdgfdlnkgleakhtllpwqctngsevg 120

QY 121 SSWAETTWISPOGIPERKVDQMDCCVYNNQYLLCSWRKPGIGVLLDTNLYNLFYWYEGLDH 180
DB 121 sswaetwyspgipetkvgmdccvynwqyllcswkpgigvlldtynllyfwyegldr 180

QY 181 ALOCVDYIKADGONICGRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQNLQIVKPLP 240
DB 181 alqcvdyikvngonigcrfpylessdykdfyicvngsssetkpirssytfqnlqivkplp 240

QY 241 PVLFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVATVENETYLTKTNE 300
DB 241 pvlctqeslyeiklwsiplgpiarpcfyeieireddtlvtvtenetytlktne 300

QY 301 TRQLCFVVRKVNIIYCSDDGIWSEWSKOCWEGEDLSKTLRLRFLWLPFGFLLILVIFVTG 360
DB 301 trqlcfvvrskvniycsddgiwsewsdkqceveellklllflilpfgfllilvifvtg 360

QY 361 LLLRPNTPYPM 372
DB 361 lllckrdsypkm 372

RESULT 12
AAW56261
ID AAW56261 standard; Protein: 315 AA.
AC AAW56261;
XX XX
DT 16-SEP-1998 (first entry)
XX XX
DE Mature interleukin-13 binding protein.
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX Homo sapiens.
XX WO9810638-A1.
XX 19-MAR-1998.
XX 10-SEP-1997; 97WO-AU00591.
XX 27-FEB-1997; 97AU-0005374.
XX 10-SEP-1996; 96AU-0002262.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
DR WPI; 1998-207062/18.
DR N-PSDB; AAV22702.
XX
PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX
PS Disclosure; Page 55-56; 69pp; English.
XX
CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for

CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
SQ Sequence 315 AA;

Query Match 85.3%; Score 1753; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.1e-163;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPQDFEIVDPGVLGYLQWQPPSLDHFKECTVEYELKYNIGSETWKTITTKN 88
DB 1 eikvnpqdfiwdpgylgylylqwgppslidhfkectveyelkynigsetwktitkn 60

QY 89 LHYKDGFDLKNKIEAKHTLLPWQCTNGSEVSSWAETTWISPOGIPETKVDQMDCVY 148
DB 61 lhykdgfdlnkgleakhtllpwqctngsevsswaettwyspgipetkvgdmdcvy 120

QY 149 NWOYLLCSWKPGIGVLLDTNLYNLFYWYEGLDHALOCVDYIKADGONICGRFPYLEASDYK 208
DB 121 nwqyllcswkpgigvlldtynllyfwyegldhalqcvdyikadgngicrpfyleasdyk 180

QY 209 DFYICVNGSSSENKPIRSSYTFQNLQIVKPLPVPVLTFTRESSCEIKLWSIPLGPIPAR 268
DB 181 dfyicvngsssenkpirssytfqnlqivkplpvpvltftressceiklwsiplgpiar 240

QY 269 CPDYEIEIREDDTTLVATVENETYLTKTNETROLCFVVRKVNIIYCSDDGIWSEWSK 328
DB 241 cfdyeieireddtlvtvtenetytlktnetrolcfvvrskvniycsddgiwsewsdk 300

QY 329 QCWEGEDLSKTLRL 343
DB 301 qcwegedlskttlrl 315

RESULT 13
AAW56260
ID AAW56260 standard; Protein: 359 AA.
XX AC AAW56260;
XX XX
DT 16-SEP-1998 (first entry)
XX XX
DE Construct containing mature interleukin-13 binding protein.
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX Homo sapiens.
XX WO9810638-A1.
XX 19-MAR-1998.
XX 10-SEP-1997; 97WO-AU00591.
XX 27-FEB-1997; 97AU-0005374.
XX 10-SEP-1996; 96AU-0002262.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
DR WPI; 1998-207062/18.
DR N-PSDB; AAV22701.
XX
PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX

```
PS Example 14; Page 52-53; 69pp; English.
XX
XX The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
XX Sequence 359 AA;
SQ
Query Match 85.3%; Score 1753; DB 19; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.6e-163;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 EIKVNPQDFEIVDGYLYLQWOPPLSLDHFKECTVEYELKYNIGSETWTKTIITKN 88
Db 45 eikvnpqdfeidvpgylylqwpplslidhfkectveyelkynigsetwtktiitkn 104
QY 89 LHYKDFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPGIPETKVDMDCVY 148
Db 105 lhykdfdlngkieakihltllpwqctngsevgsswaettywispqipetkvqmdcvy 164
QY 149 NWQYLLCSWKPGIGVLLDTNVLNFWYEGDLHALQCVDIKADGONIGCRPPYLEADYK 208
Db 165 nwqyllcskwpgigvlltdnynlfnwyegdlhalqcvdikadgongicrpfyleasyk 224
QY 209 DFYICVNGSSENKPIRSSYFTFQIQNIVKPLPPVYLATFTRESSCEIKLWSIPLGPIPAR 268
Db 225 dfyicvngssenkpirssyftfqlnqvkipppvyltftressceiklwsiplgpi 284
QY 269 CFDYIEIREDDTLVATVENETVLTNTRQLCFVWSKVNIIYCSDDGINSEWSDK 328
Db 285 cfdyieireddtlvatvenetvlttntrqlcfvwsrskvniiycsddginsesdk 344
QY 329 QCWEGEDLSKKTLLR 343
Db 345 qcwegedlskktllr 359
RESULT 14
AAW35294
ID AAW35294 standard; Protein; 383 AA.
XX
AC AAW35294;
XX
XX 27-MAR-1998 (first entry)
XX
XX Murine IL-13 binding chain of the IL-13 receptor.
XX
XX Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
KW allergy; asthma; immune complex disorder.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
FT /label= signal_sequence
FT /note= "putative"
FT 22..383
FT /label= mature_protein
FT 22..334
FT /label= extracellular_domain
FT 335..356
FT /label= transmembrane_domain
FT 357..383
FT /label= intracellular_domain
XX
XX WO9731946-A1.
PN
XX
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PD 04-SEP-1997.
XX
XX 28-FEB-1997; 97WO-US03124.
XX
XX 01-MAR-1996; 96US-0609572.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
XX Wood C;
XX
XX WPI; 1997-448632/41.
XX
XX N-PSDB; AAT75213.
XX
XX New nucleic acid encoding interleukin-13 receptor binding chain and
XX transformed cells - proteins, antibodies and inhibitors, for
XX treating immunoglobulin E-mediated diseases, e.g. Graves disease,
XX and in diagnosis
XX
XX Claim 11; Pages 30-31; 49pp; English.
XX
XX The present sequence represents the murine interleukin-13 (IL-13) binding
XX chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
XX mediator of the known biological activities of IL-13. Recombinant
XX IL-13bc proteins, and antibodies raised against them, are used to
XX inhibit the binding of IL-13 to its receptor. They are particularly used
XX to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
XX disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
XX They are also used to treat immune deficiency (particularly in
XX haematopoietic progenitor cells), cancer etc., and to increase macrophage
XX activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
XX with such activity is combined with IL-13bc and the mixture applied,
XX in vivo, to a cell expressing at least one chain of the IL-13 receptor
XX other than IL-13bc. IL-13bc can also be used in diagnosis to detect
XX expression of IL-13, its receptor or binding chain, and to raise specific
XX antibodies which may be useful for treating some tumours.
XX
XX Sequence 383 AA;
XX
Query Match 58.1%; Score 1194.5; DB 18; Length 383;
Best Local Similarity 58.9%; Pred. No. 3e-108;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
QY 1 MAFVCLAIGCLYTLFTLSTFGCTSSDTEIKVNPQDFEIVDPPGVLYLQWOPPLSLD 60
Db 1 mafv--hircclfclitctitgys----lekvnpqdfeidpbgllgyllylqwkppvvie 54
QY 61 HFKECTVEYELKYNIGSETWTKTIITKNLHYKDFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
Db 55 kfgctleyelkynrvnsvdskwtiitnlykdgfdlnkgiegkirthlsehtngsevg 114
QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNVLNFWYEGDLH 180
Db 115 spwleasygisdegslеткиqmkclynnwqylvcswkpgtkvtsdntymtfvfyegldh 174
QY 181 ALCQVDYIKADGONIGCRFPVYLEADYKDFYICVNGSSENKPIRSSYFTFQIQNIVKPLP 240
Db 175 alqcadylqhdeknvgcklsnldssdykdficvngsskileprrssyvcfqlnqvklp 234
QY 241 PVYLFTFTRESSCEIKLWSIPLGPIPARCFDYIEIREDDTLVATVENETVLTNTRQLCFV 300
Db 235 pefihisvensidirmkwstpggiprcrctyeyevireddiswesatdkndmklrrane 294
QY 301 TROLCFVVRSKVNIIYCSDDGINSEWSDKQWEGEDLSKKTLLRFLWLPFGFILLIVFTVG 360
Db 295 sedlcffvrckvniycaddgiwsewseecwgytgpdkii-fivpvcclffifillilic 353
QY 361 LLRLKPNTPYK 372
Db 354 livekeepeptci 365
```

RESULT 15

AAV95295
ID AAV95295 standard; Protein; 383 AA.

XX
AC AAV95295;

XX
DT 12-SEP-2000 (first entry)

XX
DE IL-13 binding chain of mouse IL-13 receptor.

XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.

XX
OS Mus musculus.

XX
FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "signal peptide"

FT Domain 22..383

FT Domain /note= "mature protein"

FT Domain 22..334

FT Domain /note= "extracellular domain; a polypeptide
comprising amino acids 22-334 is
specifically claimed in Claim 11(b)"

FT Domain 335..356

FT Domain /note= "transmembrane domain"

FT Domain 357..383

FT Domain /note= "intracellular domain; a polypeptide
comprising amino acids 257-383 is
specifically claimed in Claim 11(c)"

XX
PN WO200036103-A1.

XX
PD 22-JUN-2000.

XX
PF 13-DEC-1999; 99WO-US29493.

XX
PR 14-DEC-1998; 98US-0211335.

XX
PA (GEMV) GENETICS INST INC.

XX
PA (UYJO) UNIV JOHNS HOPKINS.

XX
PI Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;

XX
PI Wills-Karp M;

XX
XX WPI; 2000-431587/37.

XX
DR N-PSDB; AAA27911.

XX
XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
asthma, Grave's disease and inflammatory conditions of the lung -

XX
PS Claim 11(a); Page 50-51; 60pp; English.

XX
XX The present sequence is that of the interleukin-13 binding chain
(IL-13bc) of the murine IL-13 receptor, as deduced from an isolated
C3H/HeJ mouse thymus cDNA clone (see AAA27911). IL-13bc is a member
of the haematopoietin receptor family that acts as a mediator of
IL-13. The invention provides methods for the recombinant
production of IL-13bc polypeptides, including claimed full-length
IL-13bc, its extracellular domain, and its intracellular domain.
IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
and IL-13 receptor inhibitors (e.g. antagonists of the interaction
of IL-13 and its receptor) can be used to treat conditions in
which IL-13 is implicated, particularly IgE-mediated conditions and
diseases including atopy, allergy, asthma, immune complex diseases
(e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
thyroiditis and Grave's disease), lung inflammation,
immunodeficiency, and cancer. Since IL-13 inhibits macrophage
activation, IL-13bc proteins can also be used to enhance macrophage

CC activation, e.g. in vaccination, treatment of mycobacterial or
CC intracellular organisms or parasite infections. IL-13bc proteins
CC may also be used to potentiate the effects of IL-13 in vitro and
CC in vivo, as diagnostic agents, and to screen for agents capable of
CC binding to IL-13bc or IL-13 receptor, or which interfere with the
CC binding of IL-13 to its receptor.

XX
SQ Sequence 383 AA;

Query Match 58.1%; Score 1194.5; DB 21; Length 383;
Best Local Similarity 58.9%; Pred. No. 3e-108;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

Qy 1 MAFVCLATGCLYTLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGVLYLQWQPPLSLD 60
Db 1 mafv--hircicflilctitgys----leikvnpqdfaildpqllglylqwkppvvie 54
Qy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLKNKGIEAKTHTLLPMQCTNGSEVQ 120
Db 55 kfgctleyelkyrnvdswkttiitrlniykdgfdlnkgiegkirthlsehtngsevg 114
Qy 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWKPGLGVLLDTNWNLFYWEGLDH 180
Db 115 spwleasygisdegslctkgdmkciyvnwqylvcswkpgktvysdtnymfwwyegidh 174
Qy 181 ALQCVDYIKADGQNIQGRFPVLEASDYKDYICVNGSSSENKPIRSSYTFQQLNTVKPLP 240
Db 175 alqcadyiqhdekvnvgcklnldssdykdficvngsklepirssytfvqlnvkvplp 234
Qy 241 PVYLTFTRESSCEIKLWSIPLGPAPRCFDYEIREDDTTLVTATVENETTYTLKTNE 300
Db 235 peflhisvensidirmkwstpggpiprcycyeyeiivreddiswesatdkndmklrrane 294
Qy 301 TRQLCFVVRKVNIIYCDDGIWSEWSKQCEGEDLSKTKTLRFLWLPFGFILILVFTVG 360
Db 295 sedlcfvrckvniycaddgiwsewseecwegytpaskii-fivpvcclffifilllc 353
Qy 361 LLRLKPNYVPM 372
Db 354 livekeepeptl 365

Search completed: September 1, 2001, 19:07:03
Job time: 70 sec

| Result No. | Query Match | Score | Query | | ID | Description |
|------------|-------------|-------|--------|----|----------|--------------------|
| | | | Length | DB | | |
| 1 | 100.0 | 1901 | 380 | 18 | AAW24972 | Human interleukin- |
| 2 | 100.0 | 1901 | 380 | 18 | AAW35295 | Human IL-13 bindin |
| 3 | 100.0 | 1901 | 380 | 18 | AAW36613 | Human zcytor2 cyto |
| 4 | 100.0 | 1901 | 380 | 19 | AAW41520 | Human HR-1 recepto |
| 5 | 100.0 | 1901 | 380 | 19 | AAW41502 | Human cytokine/pep |
| 6 | 100.0 | 1901 | 380 | 19 | AAW33603 | Homo sapiens HR-1 |
| 7 | 100.0 | 1901 | 380 | 21 | AAV95296 | IL-13 binding chai |
| 8 | 100.0 | 1901 | 380 | 22 | AAV72136 | Human interleukin |
| 9 | 100.0 | 1901 | 380 | 22 | AAW29748 | Human IL-13 recept |
| 10 | 98.6 | 1875 | 380 | 18 | AAW36614 | Human zcytor2 cyto |
| 11 | 92.2 | 1753 | 315 | 19 | AAW56261 | Mature interleukin |

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are designated for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunoassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLFTTFCGCTSSDTEIKVNPDPQFEIVDPGYLYLQWPPPLSLD 60
 DB 1 mafvclaigcllytlfttfcgctssdteikvnpdpqfdevdpgylylylqwpplslid 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynrigsetwktititknhykdgfdlnkgeakihltllpwqctngsevq 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
 DB 121 sswaettywispgqipetkvdmdcvynnyqyllcswkpgigvlltdntynlfiywegldh 180
 QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadqngicrfpyleasdykdfyicvngsenkpirssyftfqlnkvkplp 240
 QY 241 PVYLFTRESSECEIKLWSIPGLPIPARCFDYEIEIREDDTTLVATVENETYTLKTNE 300
 DB 241 pvylyftressceiklwsipglpiparcfdyeieireddtllvatvenetytlktne 300
 QY 301 TROLCFVVRKVNIIYCSDDGIWSEWSKQCWGEDSLSKKTLRL 343
 DB 301 trqlcfvvrskvniiycsddgiwsewsdkqcwgedlskktllr 343

RESULT 2
 ID AAW35295
 XX AAW35295 standard; Protein; 380 AA.
 AC AAW35295;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Human IL-13 binding chain of the IL-13 receptor.
 XX
 KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25

FT /label= signal_sequence
 FT /note= "putative"
 FT Protein 26..380
 FT /label= mature_protein
 FT Domain 26..341
 FT /label= extracellular_domain
 FT Domain 342..362
 FT /label= transmembrane_domain
 FT Domain 363..380
 FT /label= intracellular_domain
 XX
 PN W09731946-A1.
 XX
 PD 04-SEP-1997.
 XX
 PF 28-FEB-1997; 97WO-US03124.
 XX
 PR 01-MAR-1996; 96US-0609572.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;
 PI
 DR WPI; 1997-448632/41.
 DR N-PSDB; AAT95214.
 XX
 PT New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transforming cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis
 XX
 PS Claim 11; Pages 34-35; 49pp; English.
 CC The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTTFCGCTSSDTEIKVNPDPQFEIVDPGYLYLQWPPPLSLD 60
 DB 1 mafvclaigcllytlfttfcgctssdteikvnpdpqfdevdpgylylylqwpplslid 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynrigsetwktititknhykdgfdlnkgeakihltllpwqctngsevq 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
 DB 121 sswaettywispgqipetkvdmdcvynnyqyllcswkpgigvlltdntynlfiywegldh 180
 QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadqngicrfpyleasdykdfyicvngsenkpirssyftfqlnkvkplp 240

Qy 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYIEIREDDTTLVTATVENETYLKTTNE 300
 Db 241 pvyitftressceiklwsipglpiparcfdyieireddtltvtatvenetylktne 300
 Qy 301 TRQLCFVVRKVNLYCSDGIGTWSWSKQCEGDELKSKTLLR 343
 Db 301 trqicfvvrskvnlycsddgiwsewskqcegedlskktllr 343

RESULT 3

AAW36613
 ID AAW36613 standard; Protein; 380 AA.

XX AC AAW36613;

DT 30-MAR-1998 (first entry)

XX Human Zcytor2 cytokine receptor protein.

XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Domain 340..363
 FT /label= transmembrane_domain
 FT Domain 364..380
 FT /label= intracellular_domain
 FT Domain 25..339
 FT /label= ligand_binding_domain

XX WO9733913-A1.

XX PD 18-SEP-1997.

XX PF 12-MAR-1997; 97WO-US04043.

XX PR 13-MAR-1996; 96US-0013345.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FU;
 PI O'Hara PJ;

XX DR WPI: 1997-470820/43.
 DR N-PSDB: AAT96782.

XX New nucleic acid encoding testis-specific cytokine receptor - useful
 PT for identification of ligands or antagonists, potentially for use as
 PT male contraceptives or for infertility treatment

XX PS Claim 2; Page 47-48; 79pp; English.

XX This sequence represents a novel ligand-binding receptor, zcytor2,
 CC which shares homology with cytokine receptors and was isolated from human
 CC placental polyA+ RNA. The resulting polypeptide is a receptor for
 CC cytokines (particularly interleukin-13) and is expressed on the surface
 CC of testicular cells, probably being involved in spermatogenesis. It can
 CC be used to detect ligands that promote proliferation and/or
 CC differentiation of such cells in cultures and may also be used to treat
 CC infertility. Antagonists of this receptor may be used to characterise
 CC ligand-receptor interactions and as male-specific contraceptives. By
 CC blocking the action of IL-13, receptor antagonists and ligand-binding
 CC this receptor can also be used to modulate immune function, e.g. in
 CC allergy and asthma, as a diagnostic to determine circulating levels of
 CC ligand and also to isolate and purify ligands. Antibodies can be used to
 CC assay circulating receptor (an abnormal level may be indicative of
 CC disease such as cancer), for labelling cells that express the receptor,
 CC and therapeutically as antagonist.

XX Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTFELISTTFCGCTSSDTEIKVNPQQDFEIVDPGVLGYLYLQWQPPLSLD 60
 Db 1 mafvclaigcltyflisttfgctssdteikvnpqqdfeiwdpgylgyllylqwgpplsld 60

Qy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHITLLPQCCTNGSEVQ 120
 Db 61 hfkectveyelkyrnigsetwktitiknlhykdgfdlnkgeakihitllpwgctngsevg 120

Qy 121 SSWAETTYWISPOGIPETKVODMDCVYVNMWYLLCSNKPGGIVLLDTNLYFYWYEGLDH 180
 Db 121 sswaettywispgipeckvqmdcvynwqyllycswnkpgigvlldtynlfywyegldh 180

Qy 181 ALQCVDIKADQONIGCFPPYLEASDYKDFYICVNGSENKPIRSSYTFQLOINIVKPLP 240
 Db 181 alqcvdyikadqonigcrfyleasdykdfyicvngssenkiprissyftqlqniwkplp 240

Qy 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYIEIREDDTTLVTATVENETYLKTTNE 300
 Db 241 pvyitftressceiklwsipglpiparcfdyieireddtltvtatvenetylktne 300

Qy 301 TRQLCFVVRKVNLYCSDGIGTWSWSKQCEGDELKSKTLLR 343
 Db 301 trqicfvvrskvnlycsddgiwsewskqcegedlskktllr 343

RESULT 4

AAW41520
 ID AAW41520 standard; Protein; 380 AA.

XX AC AAW41520;

DT 22-JUN-1998 (first entry)

XX Human HR-1 receptor.

XX HR-1 receptor; human; cytokine; infection; asthma; allergy;
 KW haematopoietic disorder; tumour; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT Protein 22..380
 FT /label= Mat_protein

XX WO9747741-A1.

XX PD 18-DEC-1997.

XX PF 12-JUN-1996; 96WO-US10262.

XX PR 12-JUN-1996; 96WO-US10262.

XX PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Appelbaum ER, Hu J;

XX WPI: 1998-052308/05.

XX DR N-PSDB: AAV04131..

XX Nucleic acid sequence encoding human cytokine peptide hormone
 PT receptor - useful to treat, prevent or diagnose, e.g. lowered
 PT resistance to infection, asthma, allergy or haematopoietic disease

XX PS Claim 13; Page 62-64; 76pp; English.

CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated the HR-1 receptor, that shows 27% identity
 CC and 52% similarity to the interleukin-5 receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
 CC human testis library. Recombinant HR-1 receptor can be expressed
 CC in claimed host cells, and used in a claimed method for identifying
 CC compounds which bind to, and activate or inhibit, it. HR-1
 CC receptor activators and agonists can be used to treat, prevent or
 CC diagnose predisposition to lowered resistance to infection, asthma,
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
 CC be used to treat conditions associated with HR-1 receptor
 CC overexpression. The antibodies can also be used to determine HR-1
 CC receptor levels, since overexpression may be diagnostic of tumours.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGTCTSSDTEIKVNPDPQFEIVDPGGLYLYLQWQPPPLSLD 60
 DB 1 mafvclaigcllytlsttgtctssdteikvnpdpqfeivdpqgllylylqwpplsl 60
 QY 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktitknlnhykgdgdlnkgleakihltllpwqctngse 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
 DB 121 sswaetywispqgipetkvqdmcdvynnwqyllylcskwpkgigvlltdnlnfywegl 180
 QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQQLQNVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
 QY 241 PVIYLTFTRESSCEIKLWSIPLGPPIPARCFDYEIREDDTTLVTATVENETYLTKTNE 300
 DB 241 pviyltfressceiklwsiplgpiiparcfdyeireddttlvtatvenetytlktne 300
 QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKKTLLR 343
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqwegedlskktllr 343

RESULT 5
 ID AAW41502
 AC AAW41502; standard; Protein; 380 AA.
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Human cytokine/peptide receptor, HR-1 receptor.
 XX
 KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
 KW neutropenia; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT Protein 22..380
 FT /label= Mat_protein
 FT /note= "Claim 14"
 XX
 PN EP812913-A2.
 XX

PD 17-DEC-1997.
 XX
 PF 04-JUN-1997; 97EP-0303815.
 XX
 PR 12-JUN-1996; 96US-0017843.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Appelbaum ER, Hu J;
 XX
 DR WP1; 1998-034974/04.
 DR N-PSDB; AAV04075.
 XX
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 XX
 PS Claim 13; Page 27-28; 34pp; English.

CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor. The amino acid sequence
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human
 CC testis cDNA library. It shows 27% amino acid identity and 52%
 CC similarity with the human interleukin-5 receptor. Also claimed are
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an
 CC agonist to the polypeptide, antibody against the polypeptide, an
 CC antagonist that inhibits the activity of the polypeptide, a process
 CC for diagnosing a disease, or a susceptibility to disease, related
 CC to expression of HR-1 receptor, and a method for identifying
 CC compounds that activate or inhibit the HR-1 receptor. HR-1
 CC receptor protein and polynucleotides can be used for research,
 CC biological, diagnosis and (gene) therapy applications, e.g. to
 CC increase resistance to infections in individuals with trauma and/or
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGTCTSSDTEIKVNPDPQFEIVDPGGLYLYLQWQPPPLSLD 60
 DB 1 mafvclaigcllytlsttgtctssdteikvnpdpqfeivdpqgllylylqwpplsl 60
 QY 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktitknlnhykgdgdlnkgleakihltllpwqctngse 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
 DB 121 sswaetywispqgipetkvqdmcdvynnwqyllylcskwpkgigvlltdnlnfywegl 180
 QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQQLQNVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
 QY 241 PVIYLTFTRESSCEIKLWSIPLGPPIPARCFDYEIREDDTTLVTATVENETYLTKTNE 300
 DB 241 pviyltfressceiklwsiplgpiiparcfdyeireddttlvtatvenetytlktne 300
 QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKKTLLR 343
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqwegedlskktllr 343

RESULT 6

CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
 CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
 CC the haematopoietin receptor family that acts as a mediator of
 CC IL-13. The invention provides methods for the recombinant
 CC production of IL-13bc polypeptides, including claimed full-length
 CC IL-13bc, its extracellular domain, and its intracellular domain.
 CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
 CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
 CC of IL-13 and its receptor) can be used to treat conditions in
 CC which IL-13 is implicated, particularly IgE-mediated conditions and
 CC diseases including atopy, allergy, asthma, immune complex diseases
 CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
 CC thyroiditis and Grave's disease), lung inflammation,
 CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
 CC activation, IL-13bc proteins can also be used to enhance macrophage
 CC activation, e.g. in vaccination, treatment of mycobacterial or
 CC intracellular organisms or parasite infections. IL-13bc proteins
 CC may also be used to potentiate the effects of IL-13 in vitro and
 CC in vivo, as diagnostic agents, and to screen for agents capable of
 CC binding to IL-13bc or IL-13 receptor, or which interfere with the
 CC binding of IL-13 to its receptor.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 21; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60
 Db 1 mafvclaigcllytlstftgctssdteikvnpqdfeiwdpgvlylylqwppplsl 60
 QY 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktititknlykdgfdlنگكieakihllpwqctngse 120
 QY 121 SSWAETTYWISPGIPETKVDMDCVYNNQYLCSWKPGIGVLLDTNMYNLFYWEGLDH 180
 Db 121 sswaetywispgipetkvdmdcvynnyqylcswkpgigvlltdtnmylnfyw 180
 QY 181 ALOCVDYIKADQNGICRFFYLEASDYKDFYICVNGSENKPIRSSFTFQLOINVRPLP 240
 Db 181 alqcvdyikadqngicrfyleasykdfyicvngssenkiprissyftqlqnvkplp 240
 QY 241 PVIYLTFTRESSCEIKLWSIPLGPIPARCFDYETEIREDDTTLVTATVENETYLKTTNE 300
 Db 241 pviyltfressceiklwsiplgpiparcfdyeteireddttlvtatvenetycl 300
 QY 301 TRQLCFVVRSKVNTYCSDDGTSWSDSKQWEGEDLSKKTLLR 343
 Db 301 trqlcfvvrskvnlcsddgtswsdsdkqwegedlskktllr 343

RESULT 8

AA72136
 ID AAY72136 standard; Protein; 380 AA.

XX
 AC AAY72136;

XX 24-APR-2001 (first entry)

XX Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).

XX Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
 KW therapy; tissue fibrosis; Schistosoma infection; surgical incision;
 KW cytostatic; wound; IL-13 related condition; allergic condition;
 KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
 KW macrophage activation.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25
 FT /label= signal_peptide
 FT Region 1..81
 FT /note= "this region is identical to the translated
 FT sequence of an expressed sequence tag (EST) identified
 FT as Y99fi0.r1 human cDNA clone 41648 5"
 FT Protein 26..380
 FT /label= Mature_human_interleukin (IL)-13_binding_chain_
 FT of_IL-13_receptor
 FT Domain 26..341
 FT /note= "Extracellular domain; this region is specifically
 FT claimed in claims 1e, 6e, 15e and 23e"
 FT Domain 342..362
 FT /note= "transmembrane domain"
 FT Domain 363..380
 FT /note= "Intracellular domain; this region is specifically
 FT claimed in claims 1f, 6f, 15f and 23f"

WO200078336-A1.

PD 28-DEC-2000.

XX 21-JUN-2000; 2000WO-US17103.

XX 21-JUN-1999; 99US-0334512.

XX (GEMY) GENETICS INST INC.
 XX (UYJO) UNIV JOHNS HOPKINS.

XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 XX Wills-Karp M;

DR WPI: 2001-080753/09.

DR N-PSDB; AAD02335.

XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
 PT in a mammalian subject, involves administering a pharmaceutical
 PT composition comprising IL-13 antagonist -

PS Claim 1a; Page 69-70; 72pp; English.

XX The invention relates to a method of treating, or inhibiting
 CC the formation of tissue fibrosis in mammals, which involves
 CC administering a pharmaceutical composition comprising interleukin
 CC (IL)-13 antagonist. The protein of the invention is useful for
 CC treating tissue fibrosis resulting from infection with Schistosoma
 CC or from healing of a wound which is a surgical incision, or
 CC inhibiting formation of tissue fibrosis which affects tissues such
 CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 CC biliary tract and gut. It is also used in the treatment or modulation
 CC of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.

CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.

XX Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60
 Db 1 mafvclaigcllytlstftgctssdteikvnpqdfeiwdpgvlylylqwppplsl 60
 QY 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120

Db 61 hfkectveyelkyrnigsetwktiitknlhkygdgfdlnkgleakihltllpwqctngsevg 120

Qy 121 SSWAETTYWISPGIPETKVDMDCVYVNWQYLLCSWRPGIGVLLDTNYNLFYWYEGLDH 180
 |||||

Db 121 sswaettywispgipetkvqmdcvyynwqyllcswkpgigvllidtnynlfywyegldh 180
 |||||

Qy 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQQLQNVKPLP 240
 |||||

Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkprrsytfqlqnvkplp 240
 |||||

Qy 241 PVYLFTRSSCEIKLWSIPLGPPIPARCFDYIEIREDDTTLVTATVENETYLTKTNE 300
 |||||

Db 241 pvyllftressceiklwsiplgppiparcfdyieireddttlvatvenetytlktne 300
 |||||

Qy 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGDLSSKTLRL 343
 |||||

Db 301 trqlcfvvrsvnlycsddgiwsewsdkqcegedlskttlrl 343
 |||||

RESULT 9

AAB29748

ID AAB29748 standard; Protein; 380 AA.

XX AC

XX AAB29748;

XX DT 23-FEB-2001 (first entry)

XX DE Human IL-13 receptor IL-13 binding chain (IL-13bc).

XX KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;

XX KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnery;

XX KW wound healing; schistosoma infection; liver; skin; muscle;

XX KW cartilage; cardiac tissue; lung tissue; uterine tissue;

XX KW intestinal tissue; vascular tissue; neural tissue.

XX OS Homo sapiens.

XX PN WO200064944-A1.

XX PD 02-NOV-2000.

XX PF 28-APR-2000; 2000WO-US11612.

XX PR 28-APR-1999; 99US-0301808.

XX PA (GEMY) GENETICS INST INC.

XX PI Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;

PI Whitters MJ, Wood C;

XX DR WPI; 2001-024676/03.

XX DR N-PSDB; AAC81416.

XX PT Treating or inhibiting tissue fibrosis resulting from infection with

PT schistosoma and wound healing involves administering interleukin-13 or

PT interleukin-4 antagonist

XX PS Claim 1; Page 76-77; 82pp; English.

XX CC The invention relates to a method of treating fibrosis in a mammal

CC by administering an interleukin-13 (IL-13) antagonist or an IL-4

CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding

CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or

CC soluble fragments thereof. The method is useful for treating or

CC inhibiting the formation of tissue fibrosis resulting from the healing

CC of a wound, including a surgical incision wound, or from infection with

CC schistosoma. The method may be used to treat fibrosis in a variety of

CC tissues, particularly liver tissue, but also skin epidermis, skin

CC endoderms, muscle, tendon, cartilage, cardiac tissue, pancreatic

CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,

CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut

CC tissue. The present sequence represents human IL-13bc.

SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 22; Length 380;

Best Local Similarity 100.0%; Pred. No. 4.6e-179; Indels 0; Gaps 0;

Matches 343; Conservative 0; Mismatches 0;

Qy 1 MAFVCLAIGCLYTLISTTFCGCTSSDTEIKVNPQDDEIVDPGVLGYLYLQWQPPLSLD 60
 |||||

Db 1 mafvclaigcltyflisttfgctssdteikvnpqdeivdpvglglylqwwqpplslid 60
 |||||

Qy 61 HFKECTVEYELKYRNIGSETWKTIIITKLNHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 |||||

Db 61 hfkectveyelkyrnigsetwktiitknlhkygdgfdlnkgleakihltllpwqctngsevg 120
 |||||

Qy 121 SSWAETTYWISPGIPETKVDMDCVYVNWQYLLCSWRPGIGVLLDTNYNLFYWYEGLDH 180
 |||||

Db 121 sswaettywispgipetkvqmdcvyynwqyllcswkpgigvllidtnynlfywyegldh 180
 |||||

Qy 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQQLQNVKPLP 240
 |||||

Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkprrsytfqlqnvkplp 240
 |||||

Qy 241 PVYLFTRSSCEIKLWSIPLGPPIPARCFDYIEIREDDTTLVTATVENETYLTKTNE 300
 |||||

Db 241 pvyllftressceiklwsiplgppiparcfdyieireddttlvatvenetytlktne 300
 |||||

Qy 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGDLSSKTLRL 343
 |||||

Db 301 trqlcfvvrsvnlycsddgiwsewsdkqcegedlskttlrl 343
 |||||

RESULT 10

AAB36614

ID AAB36614 standard; Protein; 380 AA.

XX AC

XX AAB36614;

XX DT 30-MAR-1998 (first entry)

XX DE Human Zcytor2 cytokine receptor protein.

XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;

XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.

XX OS Homo sapiens.

XX PN WO9733913-A1.

XX PD 18-SEP-1997.

XX PF 12-MAR-1997; 97WO-US04043.

XX PR 13-MAR-1996; 96US-0013345.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;

PI O'Hara PJ;

XX DR WPI; 1997-470820/43.

XX DR N-PSDB; AAT96783.

XX PT New nucleic acid encoding testis-specific cytokine receptor - useful

PT for identification of ligands or antagonists, potentially for use as

PT male contraceptives or for infertility treatment

XX PS Claim 1; Page 51-53; 79pp; English.

XX CC This sequence represents a novel ligand-binding receptor, Zcytor2, which

CC shares homology with cytokine receptors and was isolated from a human

CC testis cDNA library. The resulting polypeptide is a receptor for

CC cytokines (particularly interleukin-13) and is expressed on the surface

of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as antagonist.

Sequence 380 AA;

Query Match 98.6%; Score 1875; DB 18; Length 380;
Best Local Similarity 99.1%; Pred. No. 1.7e-176;
Matches 340; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTFGCTSSDTEIKVNPDPDFEIVDPGVLYLQWQPPLSLD 60
DB 1 mafvclaigcltytlftstfgctssdteikvnpdpdfeivdpgylylqwpplslid 60
QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
DB 61 hfkeytveyelkyrnigsetwktiitknlhykdgfdlnkgleakihtllpwqctngsevq 120
QY 121 SSWAETTWISPOGIPETKPVQDMDCVYVNWQYLLCSWKPFGIGVLLDTNLYFWYEGLDH 180
DB 121 sswaettwispgipetkvpqdmcdvynwqyllcswpfgigvlldtynlfwyegldl 180
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKVRPLP 240
DB 181 alqcvdyikadgqnigcrfyleasydkdfyicvngsssenkpirssyftfqlqnlvklp 240
QY 241 PVLFTTRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
DB 241 pvlfttressceiklwgipigpiparcfdyeieireddtllvtatvenetytlktne 300
QY 301 TROLCFVVRKVNICYSDGDIWSEWSKQCEGEDLSKKTLLR 343
DB 301 trqlcfvvrskvnicysdgdiwsewsdkqcegedlskktllr 343

RESULT 11
AAW56261
ID AAW56261 standard; Protein; 315 AA.
XX AC AAW56261;
XX AC AC
XX DT 16-SEP-1998 (first entry)
XX DE Mature interleukin-13 binding protein.
XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.
XX OS Homo sapiens.
XX PN W09810638-A1.
XX PD 19-MAR-1998.
XX PF 10-SEP-1997; 97WO-AU00591.
XX PR 27-FEB-1997; 97AU-0005374.
XX PR 10-SEP-1996; 96AU-0002262.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX FI

DR WPI; 1998-207062/18.
DR N-PSDB; AAV22702.
XX PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX PS Disclosure; Page 55-56; 69pp; English.
XX CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.

XX SQ Sequence 315 AA;

Query Match 92.2%; Score 1753; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDPDFEIVDPGVLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIITKN 88
DB 1 eikvnpdpdfeivdpgylylqwpplslidhfkeytveyelkyrnigsetwktiitkn 88
QY 89 LHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQSSWAETTWISPOGIPETKPVQDMDCVY 148
DB 61 lhykdgfdlnkgleakihtllpwqctngsevgsswaettwispgipetkvdmdcvy 120
QY 149 NWQYLLCSWKPFGIGVLLDTNLYFWYEGLDHALQCVDYIKADGONIGCRFPYLEASDYK 208
DB 121 nwqyllcswpfgigvlldtynlfwyegldhalqcvdyikadgqnigcrfyleasydk 180
QY 209 DFYICVNGSSSENKPIRSSYFTFOLQNIKVRPLPVLFTTRESSECEIKLWSIPLGPIPAR 268
DB 181 dfyicvngsssenkpirssyftfqlqnlvklpvpvlttressceiklwsipigp 240
QY 269 CFYEIEIREDDTTLVTATVENETYTLKTTNETQLCFVVRKVNICYSDGDIWSEWSK 328
DB 241 cfyeieireddtllvtatvenetytlkttnetqlcfvvrskvnicysdgdiwsewsdk 300
QY 329 QCWEGEDLSKKTLLR 343
DB 301 qcwgedlskktllr 315

RESULT 12
AAW56260
ID AAW56260 standard; Protein; 359 AA.
XX AC AAW56260;
XX AC AC
XX DT 16-SEP-1998 (first entry)
XX DE Construct containing mature interleukin-13 binding protein.
XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.
XX OS Homo sapiens.
XX PN W09810638-A1.
XX PD 19-MAR-1998.
XX PF 10-SEP-1997; 97WO-AU00591.
XX PR 27-FEB-1997; 97AU-0005374.
XX PR 10-SEP-1996; 96AU-0002262.
XX XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
 PI WPI; 1998-207062/18.
 XX N-PSDB; AAV22701.
 DR
 XX New isolated interleukin-13 binding protein - used to develop
 PT products for therapy e.g. for allergic conditions such as asthma or
 PT for diagnosis or detection
 XX
 XX Example 14; Page 52-53; 69pp; English.
 PS
 XX The IL-13 binding protein and related therapeutic molecules can be used
 CC in the antagonism of at least one IL-13 activity. They can be used for
 CC treating IL-13 mediated conditions such as certain allergic conditions
 CC such as asthma or to inactivate locally administered IL-13 after IL-13
 CC treatment. The products can also be used as diagnostic agents, e.g. for
 CC detecting autoimmune diseases. The antibodies can also be used for
 CC immunotherapy and may also be used as a diagnostic tool.
 XX
 XX Sequence 359 AA;
 SQ

Query Match 92.2%; Score 1753; DB 19; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.6e-164;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPPODFEIVDPGGLYGLYLQWQPLSLDHFKECTVEYELKYRNIGSETWKTIIITKN 88
 DB 45 elkvnppqdfelvdpgylyglwqplslsdhfkectveyelkyrnigsetwktliitkn 104
 QY 89 LHYKDGFDLNGIEAKIHTLLPWOCTNGSEVSSWAETTYWISPOGIPETKVQDMDCVY 148
 DB 105 lhykdgfdlنگieakihtllpwctngsevsqswaettywispgipetkvqdmcdvyy 164
 QY 149 NWQYLLCSWKPGIGVLLDTNLYNLFYWGDLHALQCVDIKADGONIGCRFPYLEADYK 208
 DB 165 nwqyllcswkpgigvlldtnynlfnlywyegldhalqcvdyikadgqngicrfpyleasdyk 224
 QY 209 DFYICVNGSSSEKPIRSSYFTFQLOINVKPLPPVYLTFTRESSCEIKLWSIPLGPIPAR 268
 DB 225 dfyicvngsssenkpirssyftfqlqnvkplppvyltftressceiklwsipigpar 284
 QY 269 CFDYIEIREDDTLTATVENETYLKTTNETQLCFWRSKVNICYSDGCIWSEWSDK 328
 DB 285 cfdyieireddtlvtatvenetyltktnetqlcfvrskvnicycsddgiwsewsdk 344
 QY 329 QCWEGEDLSKTKLLR 343
 DB 345 qcwgedlsktkllr 359

RESULT 13
 AAW36616
 ID AAW36616 standard; Protein; 372 AA.
 XX AC AAW36616;
 XX 30-MAR-1998 (first entry)
 XX DT
 XX Celebus macaque Zcytor2 protein.
 XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 XX OS Macaque sp.
 XX FH Key Location/Qualifiers
 FT Protein 1..372
 FT /label- Zcytor2
 FT /note- "partial protein sequence"
 XX

PN WO9733913-A1.
 XX 18-SEP-1997.
 XX 12-MAR-1997; 97WO-US04043.
 XX 13-MAR-1996; 96US-0013345.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 PI O'Hara PJ;
 XX WPI; 1997-470820/43.
 DR N-PSDB; AAT96784.
 XX New nucleic acid encoding testis-specific cytokine receptor - useful
 PT for identification of ligands or antagonists, potentially for use as
 PT male contraceptives or for infertility treatment
 XX
 XX Example 4; Page 56-57; 79pp; English.
 PS
 XX This sequence represents a novel ligand-binding receptor, Zcytor2,
 CC which shares homology with cytokine receptors and is isolated from
 CC testis tissue obtained from a Celebus macaque. The resulting polypeptide
 CC is a receptor for cytokines (particularly interleukin-13) and is
 CC expressed on the surface of testicular cells, probably being involved in
 CC spermatogenesis. It can be used to detect ligands promoting proliferation
 CC and/or differentiation of such cells in cultures and may also be used to
 CC treat infertility. Antagonists of this receptor may be used to
 CC characterise ligand-receptor interactions and as male-specific
 CC contraceptives. By blocking the action of IL-13, receptor antagonists and
 CC ligand-binding this receptor can also be used to modulate immune
 CC function, e.g. in allergy and asthma, as a diagnostic to determine
 CC circulating levels of ligand and also to isolate and purify ligands.
 CC Antibodies can be used to assay circulating receptor (an abnormal level
 CC may be indicative of disease such as cancer), for labelling cells that
 CC express the receptor, and therapeutically as antagonist.
 XX
 XX Sequence 372 AA;
 SQ

Query Match 91.5%; Score 1739; DB 18; Length 372;
 Best Local Similarity 93.3%; Pred. No. 4.1e-163;
 Matches 319; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTTFCGTSSTSDTEIKVNPQDFEIVDPGVLGYLYLQWQPLSLD 60
 DB 1 mafvylairclctflisttfgtstsdtelkvnppqdfelvdpgylglylqwgplslid 60
 QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGIEAKIHTLLPWOCTNGSEVQ 120
 DB 61 nfkectveyelkyrnigsetwtiitknlhykdgfdlنگieakihtllpwctngsevq 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYINWQYLLCSWKPGIGVLLDTNLYNLFYWGDLH 180
 DB 121 sswaetywispgipetkvqdmcdvynwqyllcswkpgigvlldtnynlfnlywyegldr 180
 QY 181 ALOCVDYIKADGONIGCRFPYLEADYKDFYICVNGSSSEKPIRSSYFTFQLOINVKPLP 240
 DB 181 alqcvdyikvqdgngicrfpyleasdykdfyicvngsssenkpirssyftfqlqnvkplp 240
 QY 241 PVIITFTRESSCEIKLWSIPLGPIPARCFDYIEIREDDTLTATVENETYLKTTNET 300
 DB 241 pvcitctqeslyelkklwsiplgpiarcfdyieireddtlvtatvenetyltktnet 300
 QY 301 TRQLCFVVRKVNICYSDGCIWSEWSDKOCWEGEDLSKTKLL 342
 DB 301 trqlcfvvrskvnicycsddgiwsewsdkqcwveellsktkll 342

RESULT 14
 AAW35294

AAW35294 standard; Protein; 383 AA.
AAW35294;
27-MAR-1998 (first entry)
Murine IL-13 binding chain of the IL-13 receptor.
Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
allergy; asthma; immune complex disorder.
Mus sp.
Key Location/Qualifiers
Peptide 1..21
Protein /label= signal_sequence
22..383 /note= "putative"
Domain /label= mature_protein
22..334 /label= extracellular_domain
Domain 335..356 /label= transmembrane_domain
Domain 357..383 /label= intracellular_domain
WO9731946-A1.
04-SEP-1997.
28-FEB-1997; 97WO-US03124.
01-MAR-1996; 96US-0609572.
(GEMY) GENETICS INST INC.
Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
Wood C;
WPI; 1997-448632/41.
N-PSDB; AAT75213.
New nucleic acid encoding interleukin-13 receptor binding chain and
transformed cells - proteins, antibodies and inhibitors, for
treating immunoglobulin E-mediated diseases, e.g. Graves disease,
and in diagnosis
Claim 11; Pages 30-31; 49pp; English.
The present sequence represents the murine interleukin-13 (IL-13) binding
chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
mediator of the known biological activities of IL-13. Recombinant
IL-13bc proteins, and antibodies raised against them, are used to
inhibit the binding of IL-13 to its receptor. They are particularly used
to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
disorders especially lupus, nephritis, thyroiditis and Grave's disease.
They are also used to treat immune deficiency (particularly in
haematopoietic progenitor cells), cancer etc., and to increase macrophage
activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
with such activity is combined with IL-13bc and the mixture applied,
in vivo, to a cell expressing at least one chain of the IL-13 receptor
other than IL-13bc. IL-13bc can also be used in diagnosis to detect
expression of IL-13, its receptor or binding chain, and to raise specific
antibodies which may be useful for treating some tumours.
Sequence 383 AA;
Query Match 62.3%; Score 1184; DB 18; Length 383;
Best Local Similarity 64.0%; Pred. No. 2.2e-108;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYFLISTFGCTSSDSTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
DB 1 mafv--hircicflilctitgys----leikvnpqdfelidpgllglylyqkpppvie 54
QY 61 HFKECTVEYELKYRNISETWKTITIKNLHYKDGFDLKNKGIEAKIHTLLPQCTNGSEVQ 120
DB 55 kfkgtleyelkyrnvdswsktiitrlniykdgfdlnkgiegkirthlsehtngsevg 114
QY 121 SSWAETTYWISPOGIPETKVDMDCVYVNWQYLLCSWPGVGLDNTYNYFYWYEGLDH 180
DB 115 spwieasygisdegslctikgmckciyynwqyivcswkpgktvysdntymffwyegldh 174
QY 181 ALQVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
DB 175 alqcadyiqhdekngvcklsnldssdykdficvngsklepirssytfqlqnvkplp 234
QY 241 PVIYLTFTRESSCEIKLWSIPLGPIPARCFDYEIREDDTLTVTATVENETTYTLTKTNE 300
DB 235 peflhisvensidirmkwstpggpiprcycteyelvireddiswesatdkndmklrrane 294
QY 301 TRQLCFVVRKVNICYSDDGIIWSEWSKQCWEG 333
DB 295 sedlofvrcvknycaddgiwsewseecweg 327
RESULT 15
AAW95295
ID AAW95295 standard; Protein; 383 AA.
XX AC AAW95295;
XX DT 12-SEP-2000 (first entry)
XX DE IL-13 binding chain of mouse IL-13 receptor.
XX KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
XX KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
XX KW immune complex disease; lupus; nephritis; thyroiditis;
XX KW Grave's disease; inflammatory; infection; therapy; antiallergic;
XX KW antinflammatory; antiasthmatic; vaccine.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Protein 22..383 /note= "mature protein"
FT Domain 22..334 /note= "extracellular domain; a polypeptide
FT 335..356 comprising amino acids 22-334 is
FT 357..383 /note= "transmembrane domain"
FT 357..383 /note= "intracellular domain; a polypeptide
FT 357..383 comprising amino acids 257-383 is
FT 357..383 specifically claimed in Claim 11(c)"
XX WO200036103-A1.
XX 22-JUN-2000.
XX 13-DEC-1999; 99WO-US29493.
XX 14-DEC-1998; 98US-0211335.
XX (GEMY) GENETICS INST INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M, Wood C;
XX Wills-Karp M;
XX

DR WPI; 2000-431587/37.
XX N-PSDB; AAA27911.
PT New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
PT asthma, Grave's disease and inflammatory conditions of the lung -
XX
PS Claim 11(a); Page 50-51; 60pp; English.
XX
CC The present sequence is that of the interleukin-13 binding chain
CC (IL-13bc) of the murine IL-13 receptor, as deduced from an isolated
CC C3H/HeJ mouse thymus cDNA clone (see AAA27911). IL-13bc is a member
CC of the haematopoietin receptor family that acts as a mediator of
CC IL-13. The invention provides methods for the recombinant
CC production of IL-13bc polypeptides, including claimed full-length
CC IL-13bc, its extracellular domain, and its intracellular domain.
CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
CC of IL-13 and its receptor) can be used to treat conditions in
CC which IL-13 is implicated, particularly IgE-mediated conditions and
CC diseases including atopy, allergy, asthma, immune complex diseases
CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
CC thyroiditis and Grave's disease), lung inflammation,
CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
CC activation, IL-13bc proteins can also be used to enhance macrophage
CC activation, e.g. in vaccination, treatment of mycobacterial or
CC intracellular organisms or parasite infections. IL-13bc proteins
CC may also be used to potentiate the effects of IL-13 in vitro and
CC in vivo, as diagnostic agents, and to screen for agents capable of
CC binding to IL-13bc or IL-13 receptor, or which interfere with the
CC binding of IL-13 to its receptor.
XX
SQ Sequence 383 AA;

Query Match 62.3%; Score 1184; DB 21; Length 383;
Best Local Similarity 64.0%; Pred. No. 2.2e-108;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAGICLYTLISTFTGCTSSDTEIKVNPQDFEIVDPQGYLYLQWQPPPLSLD 60
DB 1 mafv--hircfcflitctitgys----leikvnpqdfelldpglglylyqkxppvvie 54

QY 61 HFKECTVEYELKYRNIGSETWKTITRNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120
DB 55 kfkgtctleyelkyrnvdswkltiitrllykdgfdlnkgeakirthisehctngsevg 114

QY 121 SSWAETTWISDQGIPEKVDQDCVYVNWQYLLCSWKPFGVGLDNTNLYFYWYEGLOH 180
DB 115 spwleasygisdegsetkldqmkcllynnwqylvcswpkgtvysdntymffwyegldh 174

QY 181 ALQCDVYTKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQIVKPLP 240
DB 175 alqcadylqhcknvgcklnldssdykdficvngsskpleirssyftvqlqivkplp 234

QY 241 PVIYLTFTRESSCEIKLWSIPLGPIPARCFDYEIREDDDTLVTATVENETYLKTTNE 300
DB 235 peflhisvensidirmkwtstpggpipprcytyelvireddiswesatdkndmkikrrane 294

QY 301 TRQLCFVYVRKNIYCSDDGIWSEWSRQCWEG 333
DB 295 sedlcfvrcvknlycaddgiwsewseeceveg 327

Search completed: September 1, 2001, 19:07:04
Job time: 71 sec

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 1, 2001, 19:08:36 ; Search time 35.33 Seconds
(without alignments)
199.901 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901

Sequence: 1 MAFVCLAIGCLTYFLISTTF.....EWSDKOCWGEDLSKTKLLR 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1901 | 100.0 | 380 | 1 | US-08-609-572-4 |
| 2 | 1901 | 100.0 | 380 | 4 | US-08-841-751-4 |
| 3 | 1901 | 100.0 | 380 | 4 | US-08-846-340-4 |
| 4 | 1184 | 62.3 | 383 | 1 | US-08-609-572-2 |
| 5 | 1184 | 62.3 | 383 | 4 | US-08-841-751-2 |
| 6 | 1184 | 62.3 | 383 | 4 | US-08-846-340-2 |
| 7 | 294.5 | 15.5 | 420 | 1 | US-07-757-390-13 |
| 8 | 294.5 | 15.5 | 420 | 1 | US-08-442-282-13 |
| 9 | 294.5 | 15.5 | 420 | 2 | US-08-442-281-13 |
| 10 | 294.5 | 15.5 | 420 | 2 | US-08-939-727-13 |
| 11 | 293.5 | 15.4 | 396 | 1 | US-07-757-390-14 |
| 12 | 293.5 | 15.4 | 396 | 1 | US-08-442-282-14 |
| 13 | 293.5 | 15.4 | 396 | 1 | US-08-442-281-14 |
| 14 | 293.5 | 15.4 | 396 | 2 | US-08-939-727-14 |
| 15 | 293 | 15.4 | 313 | 3 | US-08-836-561-106 |
| 16 | 292 | 15.4 | 335 | 1 | US-07-947-130-2 |
| 17 | 292 | 15.4 | 335 | 1 | US-08-421-822-2 |
| 18 | 292 | 15.4 | 335 | 1 | US-08-421-823-2 |
| 19 | 285 | 15.0 | 427 | 4 | US-08-969-125-9 |
| 20 | 229 | 12.0 | 315 | 1 | US-07-757-390-8 |
| 21 | 229 | 12.0 | 315 | 1 | US-08-442-282-8 |
| 22 | 229 | 12.0 | 315 | 1 | US-08-442-281-8 |
| 23 | 229 | 12.0 | 315 | 2 | US-08-939-727-8 |
| 24 | 229 | 12.0 | 332 | 1 | US-07-757-390-7 |
| 25 | 229 | 12.0 | 332 | 1 | US-08-442-282-7 |
| 26 | 229 | 12.0 | 332 | 1 | US-08-442-281-7 |
| 27 | 229 | 12.0 | 332 | 2 | US-08-939-727-7 |

Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-572-4

Query Match 100.0%; Score 1901; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAFVCLAIGCLTYFLISTTFGCTSSSDTEIKVNPQDFEIVDPGYLVLYLQWQPPLSLD 60

Db 1 MAFVCLAIGCLYTLISTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYRIGSETWKTITTKNLHYKDGFDLNGKEAKIHTHTLLPQCCTNGSEVQ 120
Db 61 HFKECTVEYELKYRIGSETWKTITTKNLHYKDGFDLNGKEAKIHTHTLLPQCCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVQDMDCVYINWQYLLCSWPKGIGVLLDTNLYNLFYWYEGLDH 180
Db 121 SSWAETTWISPOGIPETKVQDMDCVYINWQYLLCSWPKGIGVLLDTNLYNLFYWYEGLDH 180
Qy 181 ALQCVDYIKADQNGICGRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQIQNIVKPLP 240
Db 181 ALQCVDYIKADQNGICGRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQIQNIVKPLP 240
Qy 241 PVLFTFTRESSCEIKLWSIPLGPAPARCFDYEIEIRDDTTLVTATVENETYLTKTNE 300
Db 241 PVLFTFTRESSCEIKLWSIPLGPAPARCFDYEIEIRDDTTLVTATVENETYLTKTNE 300
Qy 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343
Db 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343

RESULT 2
US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/841.751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-751-4

Query Match 100.0%; Score 1901; DB 4; Length 380;

Best Local Similarity 100.0%; Pred. No. le-186;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIGCLYTLISTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLISTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYRIGSETWKTITTKNLHYKDGFDLNGKEAKIHTHTLLPQCCTNGSEVQ 120
Db 61 HFKECTVEYELKYRIGSETWKTITTKNLHYKDGFDLNGKEAKIHTHTLLPQCCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVQDMDCVYINWQYLLCSWPKGIGVLLDTNLYNLFYWYEGLDH 180
Db 121 SSWAETTWISPOGIPETKVQDMDCVYINWQYLLCSWPKGIGVLLDTNLYNLFYWYEGLDH 180
Qy 181 ALQCVDYIKADQNGICGRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQIQNIVKPLP 240
Db 181 ALQCVDYIKADQNGICGRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQIQNIVKPLP 240
Qy 241 PVLFTFTRESSCEIKLWSIPLGPAPARCFDYEIEIRDDTTLVTATVENETYLTKTNE 300
Db 241 PVLFTFTRESSCEIKLWSIPLGPAPARCFDYEIEIRDDTTLVTATVENETYLTKTNE 300
Qy 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343
Db 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343
RESULT 3
US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-846-340-4

Query Match 100.0%; Score 1901; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLFISTTFCGTSSTSDTEIKVNPDPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLFISTTFCGTSSTSDTEIKVNPDPQDFEIVDPGVLGYLYLQWQPPLSLD 60

Qy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120

Qy 121 SSWAETTWISPOGIPETKVDMDCVYNNQYLCSKPGIGVLLDTNINFLFYWEGLDH 180
Db 121 SSWAETTWISPOGIPETKVDMDCVYNNQYLCSKPGIGVLLDTNINFLFYWEGLDH 180

Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQQLNIVKPLP 240
Db 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQQLNIVKPLP 240

Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLTKTNE 300
Db 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLTKTNE 300

Qy 301 TROLCFVVRKVNIVCYSDGIGWSEWSKQCEGEDLSKKTLLR 343
Db 301 TROLCFVVRKVNIVCYSDGIGWSEWSKQCEGEDLSKKTLLR 343

RESULT 4

US-08-609-572-2
; Sequence 2, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-609-572-2

Query Match 62.3%; Score 1184; DB 1; Length 383;
Best Local Similarity 64.0%; Pred. No. 2e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

Qy 1 MAFVCLAIGCLYTLFISTTFCGTSSTSDTEIKVNPDPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFV--HRCICFLCITITIGTIS----LEIKVNPDPQDFEILDPLGLGYLYLQWKPVPVIE 54

Qy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120

Qy 121 SSWAETTWISPOGIPETKVDMDCVYNNQYLCSKPGIGVLLDTNINFLFYWEGLDH 180
Db 121 SSWAETTWISPOGIPETKVDMDCVYNNQYLCSKPGIGVLLDTNINFLFYWEGLDH 180

Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQQLNIVKPLP 240
Db 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQQLNIVKPLP 240

Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLTKTNE 300
Db 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLTKTNE 300

Qy 301 TROLCFVVRKVNIVCYSDGIGWSEWSKQCEGEDLSKKTLLR 343
Db 301 TROLCFVVRKVNIVCYSDGIGWSEWSKQCEGEDLSKKTLLR 343

RESULT 5

US-08-841-751-2
; Sequence 2, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:

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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 383 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-841-751-2

Query Match          62.3%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 2e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCYLTFLISTFCTSSDTEIKVNPQDPEIYVDPGVLGYLYLOWPPPLSLD 60
DB 1 MAFV--HIRCLCFILLCTITGYS-----LEIKVNPQDPEILDPLGLLYLQWPPVIVIE 54

QY 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNGKTEAKIHTLLPWQCTNGSEVQ 120
DB 55 KFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNGKTEAKIHTLSEHCINGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGLVLDNTNLYFYWVEGLDH 180
DB 115 SPWIEASGISDEGSLKTIQDMKCIYNNWQYLLCSWKPGLVLDNTNLYFYWVEGLDH 174

QY 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFICVNGSSKPKIRSSYTFQIQNVKPLP 240
DB 175 ALQCADYLQHDKNVCKLSNLDSSDYKDFICVNGSSKPKIRSSYTFQIQNVKPLP 234

QY 241 PVIYLTFTRESCEIKLWSIPLGPPIPARCFDYEIREDDTTLVATVENETYLKTTNE 300
DB 235 PEFUHSIVENSIDIRMKWSTPGGPIPPRCYTYEIVREDDISWESATDKNDKMLKRRANE 294

QY 301 TRQLCFVVRKVNICYSDGDIWSEMSDKQWEG 333
DB 295 SEDLCFFVRCKVNICYADGDIWSEMSDEECWEG 327

RESULT 6
US-08-846-340-2
; Sequence 2, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A. 32,724
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: G15268

;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 498-8224
;   TELEFAX: (617) 876-5851
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 383 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-846-340-2

Query Match          62.3%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 2e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCYLTFLISTFCTSSDTEIKVNPQDPEIYVDPGVLGYLYLOWPPPLSLD 60
DB 1 MAFV--HIRCLCFILLCTITGYS-----LEIKVNPQDPEILDPLGLLYLQWPPVIVIE 54

QY 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNGKTEAKIHTLLPWQCTNGSEVQ 120
DB 55 KFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNGKTEAKIHTLSEHCINGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGLVLDNTNLYFYWVEGLDH 180
DB 115 SPWIEASGISDEGSLKTIQDMKCIYNNWQYLLCSWKPGLVLDNTNLYFYWVEGLDH 174

QY 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFICVNGSSKPKIRSSYTFQIQNVKPLP 240
DB 175 ALQCADYLQHDKNVCKLSNLDSSDYKDFICVNGSSKPKIRSSYTFQIQNVKPLP 234

QY 241 PVIYLTFTRESCEIKLWSIPLGPPIPARCFDYEIREDDTTLVATVENETYLKTTNE 300
DB 235 PEFUHSIVENSIDIRMKWSTPGGPIPPRCYTYEIVREDDISWESATDKNDKMLKRRANE 294

QY 301 TRQLCFVVRKVNICYSDGDIWSEMSDKQWEG 333
DB 295 SEDLCFFVRCKVNICYADGDIWSEMSDEECWEG 327

RESULT 7
US-07-757-390-13
; Sequence 13, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
```

```
;
;
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-07-757-390-13

Query Match          15.5%; Score 294.5; DB 1; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

Qy 27 DTEKVNPPQDFEIVDPGVLGYLYLQWQPLSLDHFKECTVEYELKYRNIGSETWTKTIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
Qy 87 KNLHYKQGFDLNKGIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKQVDMDCV 146
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTGVVNLCT 135
Qy 147 -----YNNQYLL-CSWKPFGIGVLLDTNINLFY---WYEGLDHALQCVDYIKAD 191
Db 136 TTTTNDNYSRLRSQVSLHCTWLVGTDAPEDTQVFLYYRGSWTE-----ECQEYSKDT 189
Qy 192 -GONIGCRFP--YLEADYKDFYICVNGSSNKPIRSYFTFQLONIYKPLPPVLTFTTR 248
Db 190 LGRNIACFPFRFTILSKGRDMLAVLVNGSSKHSAIRPPDQLFALHAIDQINPPLNVTAEI 249
Qy 249 ESSCEIKLKWISPLGPAPCFDYEIEIREDDTTLVATVENETYLTKTTNETROLCFVW 308
Db 250 EGT-RLSIQWEKPYSAFPIHCFDYEIVKHNTNRNGVLOIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RAAVSSMCREAGLWSEWS-QPIYYGVNDEHK 337

RESULT 8
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
```

```
;
;
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-442-282-13

Query Match          15.5%; Score 294.5; DB 1; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

Qy 27 DTEKVNPPQDFEIVDPGVLGYLYLQWQPLSLDHFKECTVEYELKYRNIGSETWTKTIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
Qy 87 KNLHYKQGFDLNKGIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKQVDMDCV 146
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTGVVNLCT 135
Qy 147 -----YNNQYLL-CSWKPFGIGVLLDTNINLFY---WYEGLDHALQCVDYIKAD 191
Db 136 TTTTNDNYSRLRSQVSLHCTWLVGTDAPEDTQVFLYYRGSWTE-----ECQEYSKDT 189
Qy 192 -GONIGCRFP--YLEADYKDFYICVNGSSNKPIRSYFTFQLONIYKPLPPVLTFTTR 248
Db 190 LGRNIACFPFRFTILSKGRDMLAVLVNGSSKHSAIRPPDQLFALHAIDQINPPLNVTAEI 249
Qy 249 ESSCEIKLKWISPLGPAPCFDYEIEIREDDTTLVATVENETYLTKTTNETROLCFVW 308
Db 250 EGT-RLSIQWEKPYSAFPIHCFDYEIVKHNTNRNGVLOIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RAAVSSMCREAGLWSEWS-QPIYYGVNDEHK 337

RESULT 9
US-08-442-281-13
; Sequence 13, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
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```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-13

Query Match 15.5% Score 294.5; DB 1; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

QY 27 DTEIKVNPQDFEIVDPGLGYLYLQWQPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
Db 25 DEKISLLPPVNFITKVGTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
QY 87 KNLHYKQDFDLNKGIEAKIHLLPWQCTNGSEVSSWAETTYWISPOGIPETKYVQDMDCV 146
Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSGTSSVNLTC 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGLDHALQCVDYIKAD 191
Db 136 TWTEDNYSRLRSYQVSLHCTWLVTGTDAPETQFLYIRYGSWTE-----ECOEYSKDT 189
QY 192 -GQNIQGRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLNIVKPLPPVLTFR 248
Db 190 LGRNIACWFPRFTILSKGRDLAVLVNGSSKSHAIRPFDQALFALHAIQINPPLNVTAEI 249
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVTATVENETTYTLKTTNETQLCFV 308
Db 250 EGT-RLSQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWSDKOCWEGEDLSK 338
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337

RESULT 10
US-08-939-727-13
; Sequence 13 Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-13

Query Match 15.5% Score 294.5; DB 2; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

QY 27 DTEIKVNPQDFEIVDPGLGYLYLQWQPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
Db 25 DEKISLLPPVNFITKVGTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
QY 87 KNLHYKQDFDLNKGIEAKIHLLPWQCTNGSEVSSWAETTYWISPOGIPETKYVQDMDCV 146
Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSGTSSVNLTC 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGLDHALQCVDYIKAD 191
Db 136 TWTEDNYSRLRSYQVSLHCTWLVTGTDAPETQFLYIRYGSWTE-----ECOEYSKDT 189
QY 192 -GQNIQGRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLNIVKPLPPVLTFR 248
Db 190 LGRNIACWFPRFTILSKGRDLAVLVNGSSKSHAIRPFDQALFALHAIQINPPLNVTAEI 249
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVTATVENETTYTLKTTNETQLCFV 308
Db 250 EGT-RLSQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWSDKOCWEGEDLSK 338
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337

RESULT 11
US-07-757-390-14
; Sequence 14 Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/757,390
;; FILING DATE: 19910910
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 7005-030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 8698864/9741
;; TELEFAX: 212 8698864/9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 396 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-07-757-390-14

Query Match 15.4%; Score 293.5; DB 1; Length 396;
Best Local Similarity 27.9%; Pred. No. 3.7e-22;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;
QY 27 DTEIKVNPQDPEIYDVGVLGYLYLQWPPPLSLDHFKECTVEYELKYRNIGSETWTKTIT 86
DB 25 DEKISLLPVPNTIKVTG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAKPEDDYETRT 82
QY 87 KNLHYKDFDLNKGTEAKHTLLPQCCTNGSEVQSSWAETTYWISQGIPEKTVQDMDCV 146
DB 83 ES---KCVTLHKGSASVRTILQ---NDHSLTSSWASAEHL-APPGSPGSIYNLTCT 135
QY 147 -----YYNWQYLL-CSWKPQIGVLLDTNYNLFY----WYEGLDHALQCVDIKAD 191
DB 136 TWTEDNYSRLRSYQVSLHCTWLVTGTDAPEDQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -QNTGCRPP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLNIVKPLPPVYLTFTTR 248
DB 190 LGRNIACTFPRTFILSKGRDWLAVLVNGSSKHSARPFQDLFALHAIDQINPLNVTAEI 249
QY 249 ESSCEIKLKWSTPLGPICARCFDYEIEIREDDTTLVTATVENETYLKTTNETROLCFVV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTMTNFAFISIIDLSDSKYDVQV 308
QY 309 RSKVNIYSDGDIWSEWSKQCEGEDLSK 338
DB 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337

RESULT 12
US-08-442-282-14
; Sequence 14, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/442,282
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/757,390
;; FILING DATE: 10-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 7005-030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 790-9090
;; TELEFAX: 212 8698864/9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 396 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-442-282-14

Query Match 15.4%; Score 293.5; DB 1; Length 396;
Best Local Similarity 27.9%; Pred. No. 3.7e-22;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;
QY 27 DTEIKVNPQDPEIYDVGVLGYLYLQWPPPLSLDHFKECTVEYELKYRNIGSETWTKTIT 86
DB 25 DEKISLLPVPNTIKVTG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAKPEDDYETRT 82
QY 87 KNLHYKDFDLNKGTEAKHTLLPQCCTNGSEVQSSWAETTYWISQGIPEKTVQDMDCV 146
DB 83 ES---KCVTLHKGSASVRTILQ---NDHSLTSSWASAEHL-APPGSPGSIYNLTCT 135
QY 147 -----YYNWQYLL-CSWKPQIGVLLDTNYNLFY----WYEGLDHALQCVDIKAD 191
DB 136 TWTEDNYSRLRSYQVSLHCTWLVTGTDAPEDQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -QNTGCRPP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLNIVKPLPPVYLTFTTR 248
DB 190 LGRNIACTFPRTFILSKGRDWLAVLVNGSSKHSARPFQDLFALHAIDQINPLNVTAEI 249
QY 249 ESSCEIKLKWSTPLGPICARCFDYEIEIREDDTTLVTATVENETYLKTTNETROLCFVV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTMTNFAFISIIDLSDSKYDVQV 308
QY 309 RSKVNIYSDGDIWSEWSKQCEGEDLSK 338
DB 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337

RESULT 13
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas

```

; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-14

```

```

Query Match      15.4%; Score 293.5; DB 1; Length 396;
Best Local Similarity 27.9%; Pred. No. 3.7e-22;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;

```

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QY 27 DPEIKVNPQDFEIVDPGLYLGVLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLLPPVNFITKVGT-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKGFGLNKGIEAKIHLLPWQCTNGSEVOSSWAETTYTISPOGIPETKVQDMDCV 146
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSAVRITLQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTCT 135
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGLDHALQCVDIKAD 191
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQFLYIRYGSWTE-----ECOEYSKDT 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQNLQIVKPLPPVLTFT 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACFPRTFILSKGRDMLAVLVNGSSKHSARIPDQLFALHAIDQINPPLNVTAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTLVATVENETTYTLTKTNETQLCFV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYVHNRNGYLQIEKLMTNAFISIIDLSDKYDVQ 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGIWSEWSKOCWEGEDLSK 338
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSMCREAGLWSEWS-QPIYVGNDEHK 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 14
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor

```

```

; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennle & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-14

```

```

Query Match      15.4%; Score 293.5; DB 2; Length 396;
Best Local Similarity 27.9%; Pred. No. 3.7e-22;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;

```

```

QY 27 DTEIKVNPQDFEIVDPGLYLGVLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLLPPVNFITKVGT-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKGFGLNKGIEAKIHLLPWQCTNGSEVOSSWAETTYTISPOGIPETKVQDMDCV 146
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSAVRITLQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTCT 135
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGLDHALQCVDIKAD 191
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQFLYIRYGSWTE-----ECOEYSKDT 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQNLQIVKPLPPVLTFT 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACFPRTFILSKGRDMLAVLVNGSSKHSARIPDQLFALHAIDQINPPLNVTAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTLVATVENETTYTLTKTNETQLCFV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYVHNRNGYLQIEKLMTNAFISIIDLSDKYDVQ 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGIWSEWSKOCWEGEDLSK 338
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSMCREAGLWSEWS-QPIYVGNDEHK 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 15
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi

```


Search completed: September 1, 2001, 19:08:36
Job time: 163 sec

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Query Match      15.4%; Score 293; DB 3; Length 313;
Best Local Similarity 28.3%; Pred. No. 2.9e-22;
Matches 90; Conservative 55; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEKVNPPDDEIVDGYLGYLQLQWQPPLSLDHFKECTVEYELKYNIGSETWTKIIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5 DEKISLLPPVNFITKVG-LAQVLLQWKPNPDQSQ-RNVNLEYQVKINAPKEDDYETRI 62
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKDGDFLNLKGIEAKIHTLLPQWCTNGSEVGSWAETTYTWSPOGIPETKYQDMDCV 146
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 63 ES---KCVTILHKGFSAVRTILQ---NDHSLLASSWASAEHL-APGSPGTSVVNLCT 115
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYP-----WYEGLDHALQCVDYIKAD 191
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 116 TTTEDNYSRLRSYQVSLHCTWLVTGTDAPETQFLYYRGSWTE-----ECQEYSKDT 169
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -QNIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYTFQIQNVKPLPPVYLIFTR 248
   | : | | | | : : : : | : | : | : | : | : | : | : | : | : | : |
Db 170 LGRNIACWFRTFLSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEI 229
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSEIKLKSIPGLGPFPARCFDYEIEIRDDTTLVTAVENETYYLTKTNTQLQCFVV 308
   | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 230 EGT-RLSIQWEKPSAPPIHCFDYEYVHIHNRNGYLQIEKLTWNAFISIDLSKYDVQV 288
   | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGIGWSEWS 326
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 289 RAAVSSMCREAGLWSEWS 306
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:26 ; Search time 24.79 Seconds
(without alignments)
465.676 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLATGCLYFLITTF.....DDGIWSEWSDKOCWGEDLS 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1 | 1873 | 100.0 | 380 | 1 | IL32_HUMAN |
| 2 | 282.5 | 15.6 | 420 | 1 | IL5R_HUMAN |
| 3 | 289.5 | 15.5 | 424 | 1 | IL31_MOUSE |
| 4 | 285 | 15.2 | 427 | 1 | IL31_HUMAN |
| 5 | 254 | 13.6 | 831 | 1 | PLRL_CHICK |
| 6 | 229 | 12.2 | 415 | 1 | IL5R_MOUSE |
| 7 | 228 | 12.2 | 831 | 1 | PLRL_MELGA |
| 8 | 210.5 | 11.2 | 830 | 1 | PLRL_COLLI |
| 9 | 202.5 | 10.8 | 369 | 1 | CYRG_HUMAN |
| 10 | 199.5 | 10.7 | 373 | 1 | CYRG_CANFA |
| 11 | 198.5 | 10.6 | 369 | 1 | CYRG_MOUSE |
| 12 | 180 | 9.6 | 379 | 1 | CYRG_BOVIN |
| 13 | 179 | 9.6 | 878 | 1 | IL3B_MOUSE |
| 14 | 165 | 8.8 | 581 | 1 | PLRL_BOVIN |
| 15 | 165 | 8.8 | 610 | 1 | PLRL_RAT |
| 16 | 160 | 8.5 | 897 | 1 | CYRB_HUMAN |
| 17 | 159 | 8.5 | 608 | 1 | PLRL_MOUSE |
| 18 | 155.5 | 8.3 | 896 | 1 | CYRB_MOUSE |
| 19 | 151 | 8.1 | 622 | 1 | PLRL_HUMAN |
| 20 | 150.5 | 8.0 | 917 | 1 | IL6B_MOUSE |
| 21 | 150 | 8.0 | 581 | 1 | PLRL_CEREL |
| 22 | 147 | 7.8 | 616 | 1 | PLRL_RABIT |
| 23 | 145.5 | 7.8 | 862 | 1 | IL2S_HUMAN |
| 24 | 133.5 | 7.1 | 400 | 1 | GMCR_HUMAN |
| 25 | 130.5 | 7.0 | 378 | 1 | IL3R_HUMAN |
| 26 | 128 | 6.8 | 630 | 1 | PLRL_ORENI |
| 27 | 126.5 | 6.8 | 874 | 1 | IL2S_MOUSE |
| 28 | 126.5 | 6.8 | 918 | 1 | IL6B_HUMAN |
| 29 | 123.5 | 6.6 | 1097 | 1 | LIFR_HUMAN |
| 30 | 113.5 | 6.1 | 1165 | 1 | LEPR_HUMAN |
| 31 | 112.5 | 6.0 | 1630 | 1 | PTPO_DROME |
| 32 | 109.5 | 5.8 | 918 | 1 | IL6B_RAT |
| 33 | 107 | 5.7 | 634 | 1 | GHR_BOVIN |

ALIGNMENTS

RESULT 1
IL32_HUMAN
ID IL32_HUMAN STANDARD; PRT; 380 AA.
AC Q14627; O00667;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13

DE BINDING PROTEIN).

GN IL13RA2 OR IL13R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Renal cell carcinoma;

RX MEDLINE=96279273; PubMed=8663118;

RA Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N.,

RA Ferrara P.;

RT "Cloning and characterization of a specific interleukin (IL)-13

RT binding protein structurally related to the IL-5 receptor alpha

RT chain.";

RL J. Biol. Chem. 271:16921-16926(1996).

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

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DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;

Query Match 100.0%; Score 1873; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
DB 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60

QY 61 HFKECTVEYELKYRNISETWTKTITKLNHYKDFDLNKGTEAKIHLLPQCTNGSEVQ 120
DB 61 HFKECTVEYELKYRNISETWTKTITKLNHYKDFDLNKGTEAKIHLLPQCTNGSEVQ 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNFWYEGLDH 180
DB 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNFWYEGLDH 180

QY 191 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFQIQNIVKPLP 240
DB 191 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFQIQNIVKPLP 240

QY 241 PVYLFTRESSECEIKLWSIPLGPPIPCFDFEIEIRDDDTLTAIVENETYLTKTNE 300
DB 241 PVYLFTRESSECEIKLWSIPLGPPIPCFDFEIEIRDDDTLTAIVENETYLTKTNE 300

QY 301 TROLQFVVRKVNIVCSDDGIWSEMSDKQWGEDLS 337
DB 301 TROLQFVVRKVNIVCSDDGIWSEMSDKQWGEDLS 337

RESULT 2
ID IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).
DE IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;

RT RT
RT RT
RL RL
RN RN
RP RP
RX RX
RA RA
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-specific alpha chain and a beta chain shared with the receptor for GM-CSF.";
RT for GM-CSF.";
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY ALTERNATIVE SPLICING
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
CC -----
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CC -----
EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A26249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A26251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; 147851; -
DR InterPro; IPR000950; -
DR InterPro; IPR002465; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420
FT DOMAIN 21 342
FT TRANSMEM 343 362
FT DOMAIN 363 420
FT CARBOHYD 35 35
FT CARBOHYD 131 131
FT CARBOHYD 216 216
FT CARBOHYD 244 244
FT VARSPLIC 333 335
FT VARSPLIC 336 420
FT VARSPLIC 333 333
FT VARSPLIC 334 420
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NDE -> FSR (IN SOLUBLE ISOFORM S1).
MISSING (IN SOLUBLE ISOFORM S1).
N -> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
Query Match 15.6%; Score 292.5; DB 1; Length 420;
Best Local Similarity 27.8%; Pred. No. 4.4e-17;
Matches 91; Conservative 58; Mismatches 143; Indels 35; Gaps 13;

QY 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLDHFKECTVEYELKYRNISETWTKTIT 86
DB 25 DEKISLLPPVNFITKVTG-LAQVLLQKPNPDQEQ-RNVNLEYQVKINAKPEDDYETRIT 82

QY 87 KNLHYKDFDLNKGIEAKIHLLPQCTNGSEVOSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES----KCVTILHKGFSAVRLTQ---NDHSLASSWASAEHLH-APPGSPGTSIVNLTCT 135
```

QY 147 -----YNNQYLL-CSWKPICIGVLLDTNLYF-----WYEGDLHALQCVDYIKAD 191
 Db 136 TTTTNDYNSRLRSQVSLHCTWLTGTDAPETQYFLYRYGSWTE-----ECQEYSKOT 189
 QY 192 -QONIGRFP--YLEASDYKDFYICVNGSSNKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
 Db 190 LGRNIACWFPRFTLSLGRDNLWSLVNNGSSKHSARIPDFQDLFALHAIQINPPLNVTAEI 249
 QY 249 ESSCEIKLWSIPGLPIPARCFDEIEIREDDTTLVATVENETYLTKTNETQLCFV 308
 Db 250 EGT-RLSQWEKPSAPFIHCFDEIVKHNRNGYLOIEKLMTNAFISIDDLKSYDVQV 308
 QY 309 RSKVNIYCSDDGIWSESDKQCEGED 335
 Db 309 RAAVSSMCREAGLWSENS-QPIYVGN 334

RESULT 3
 ID I131_MOUSE STANDARD; PRT; 424 AA.
 AC O09030;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).
 GN IL13RA1 OR IL13RA OR IL13R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96133964; PubMed-8552669;
 RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
 RA Willson T.A.;
 RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
 CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).
 CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; S80963; AAB50695.1; -;
 DR MGD; MGI:105052; I113ra.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 424 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
 FT DOMAIN 26 340 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 341 364 POTENTIAL.
 FT DOMAIN 365 424 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 37 100 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 44 93 POTENTIAL.

FT DISULFID 132 142 BY SIMILARITY.
 FT DISULFID 171 183 BY SIMILARITY.
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;

Query Match 15.5%; Score 289.5; DB 1; Length 424;
 Best Local Similarity 25.8%; Pred. No. 7.8e-17;
 Matches 93; Conservative 63; Mismatches 131; Indels 73; Gaps 17;

QY 8 IGCLYTFELIST-TEGCTSSSDTEIKVNPQQDFEIVDPGYGLYLOQPPPLSLDHFRECT 66
 Db 7 LGELLVLLLTATVGVAAA---TEVQPPVTNLSVSVENCTIITWSPPGAS--PNCT 61
 QY 67 VEY-----ELKYNIGSETWKTITITKLNHYKDFDLNKGIEAKIHTLLPWQCT-NGSEVQ 120
 Db 62 LRYFSEHFDQDDKKIAPET-----HRKEELPLDEKICLVGS---QCSANESEK 108
 QY 121 SSWAETTYWIS-POGIPETKVQDMQDVYVYNNQYLLCSWKPGIGVLLDTNLYNLFYWGELD 179
 Db 109 SPLVKKC--ISPPGDPESAATVETKLCIWHNLSYMKCSWLPGRNTSPDTHLYTYWYSSLE 166
 QY 180 HALOCVDYIRADGONIGCRFPYLEAS---DYKDFYICVNGSSSENKPIRSYFTFQNLQIV 236
 Db 167 KSRQC-ENIYREGQHIACSPKLTKEPSEFQNVQIMVKDNAGK--IRPSKIVSLTSYV 223
 QY 237 KPLPPVLTITRESSCEIKLWSIPGLPIPARCFDEIEIR----- 277
 Db 224 KPDP-PIKHLKLLKALLVQKNPN-FRSCLTYEVVNTQDHRNILEVEDKCON 281
 QY 278 -EDDTL-----VTATVENETVTLTKTNETQLCFVVRKSVNIYCSDDGIWSESDKQ 329
 Db 282 SESDRNMEGTSFQLPGVLADAVYTVRVVKTNLCF-----DDNKLWSDWSEAQ 331

RESULT 4
 ID I131_HUMAN STANDARD; PRT; 427 AA.
 AC P78552; Q99656; Q95646;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1).
 GN IL13RA1 OR IL13RA OR IL13R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE-97165986; PubMed-9013879;
 RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
 RA Ferrara P.;
 RA "Cloning of the human IL-13R alpha chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex."
 RL FEBS Lett. 401:163-166(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
 RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
 RA Eugster H.P., Bonnefoy J.Y.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-T-cell;


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FT DOMAIN 25 122 FIBONECTIN TYPE-III.
FT DOMAIN 123 225 FIBONECTIN TYPE-III.
FT DOMAIN 228 325 FIBONECTIN TYPE-III.
FT DOMAIN 326 428 FIBONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 1C4E7591DCADB9 CRC64;

Query Match 13.6%; Score 254; DB 1; Length 831;
Best Local Similarity 27.3%; Pred. No. 1.6e-13;
Matches 93; Conservative 48; Mismatches 158; Indels 42; Gaps 14;

Qy 18 TTEGCTSSDTEIKVN--PQDFE---IVDPG-----YLGVLVLOWQPPLSL 59
Db 97 TTFNLTATNEIGNSDPQVDVTSVQPGSNVLFETKRSANIMYLWAKWSPPLLA 156
Qy 60 DHFKECTVEYELKYNIGSETWKTITKNLHYKQDGLNKGIEAKIHTLLPWQCTNGSEV 119
Db 157 DASSNHYHYELRIKPEKEWETI---SVGVQVQCKINR-LNAGMRVYVQVRCILDPE 212
Qy 120 QSSWAETTYWISPOG-IPETKVQDMCVYNNQYLLCSWKPGIGVLLDTNLFYFWYEG 178
Db 213 WSEWSSERHILIPQSPPEKPTIIFKRSPEKETFTCWKPKGLDGGHPTNTLLYSKEGE 272
Qy 179 DHALQCVYIKADGONIGCRPPYLEASDYKDFYICVNGSSSENKPIRSSYFFQLQNIKVP 238
Db 273 EQVIECPDY-RFAPGN-SCYFDKHTSTWYITNITVRATNEMGNSDPHYVDVTVIQP 330
Qy 239 LPPVYLTTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR---EDDTTLVTATVEN 290
Db 331 DPPVNVTLKPKPKINRKPVLVLTWSPPLADVRSGWLTLEVLRLKPEGEWEWEIFVQ 390
Qy 291 ET-YTLKTTNETRQLCFVVRKVNYSDD--GIWSEWSK 328
Db 391 QTOYKMFSLNPGKKYI-----IQHCKPDHGHGWSSENSE 425

RESULT 6
IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).
GN IL5R OR IL5R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takatsuki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RT "Molecular cloning and expression of the murine interleukin-5
receptor."
RL EMO J. 9:4367-4374(1990).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
ON B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D90205; BAA14231.1; -
DR PIR; S12357; S12357.
DR MGI; MGI:96558; IL5ra.
DR InterPro; IPR000950; -.
DR InterPro; IPR002465; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 339 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 340 361 POTENTIAL.
FT DOMAIN 362 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 152 BY SIMILARITY.
FT DISULFID 179 193 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 12.2%; Score 229; DB 1; Length 415;
Best Local Similarity 24.8%; Pred. No. 8.1e-12;
Matches 79; Conservative 56; Mismatches 135; Indels 48; Gaps 13;

Qy 34 PQDQPEIVDPGVGLYLYLQWQPPLSLDHFKECTVEYELKYNIGSETWKTITKNLHYKD 93
Db 29 PPNVETIKATG-LAQVLLHWDNPQDEQ-RHVDLEHYHKINAPQDEYDTRKTES--KC 83
Qy 94 GFDLNKGIEAKIHTLLPWQCTNGSEVQSWAETTYWISPOGIPETKVQDMCVYNN---- 149
Db 84 VPLHEGFAASVRTLK---SSHTTLASSWSVAEL-KAPPGSPGTSVNLCTCTHTVYSS 139
Qy 150 -----WQY-LLCSWKPGIGVLLDTNLYNFYWEGLDHALQCVDIK-ADGONIGCRPP- 200
Db 140 HTHLRPYQVSLRCTLWLVGKDAPEDTQYFLYRFGVLTE--KCQEYSRDALNNTACWFP 197
Qy 201 -YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIKVPVLTFTRESSCEIKLWS 259
Db 198 TFINSKGFEQLAVHINGSKRAAIKPFQDLSPDLAQVNPPRNVTVIESN-SLIQWE 256
Qy 260 IPLGPIPARCFDYEIEIREDD-----TTLVTATVENETVTLKTTNETRQLCFV 308
Db 257 KPLSAFPDCHFCNYELKIYNTKNGHIQKELIANKFISKIDVDVTSIQ-----V 305
Qy 309 RSKVNIYSDDGINSEWS 326
Db 306 RAAVSSPCRMFGRWGEWS 323

RESULT 7
PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 CC NCBI_TaxID=9103;
 [1]
 RN SEQUENCE FROM N.A.
 RP
 RC TISSUE=Kidney;
 RC MEDLINE=97057891; PubMed=8902221;
 RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
 RT "Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RT gallopavo.";
 RL Biol. Reprod. 55:1081-1090(1996).
 [2]
 RN
 RP
 RC TISSUE=Ovary;
 RC plitts G.R., You S.K., Foster D.N., el Halawani M.E.;
 RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS,
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC use by non-profit institutions as long as its content is in no way
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 CC
 CC EMBL; L76587; AAB01544.1; -;
 CC EMBL; U22947; AAY75038.1; -;
 CC EMBL; U22924; AAY75039.1; -;
 CC HSP; P16471; IBP3.
 CC
 CC InterPro: IPR000950; -;
 CC InterPro: IPR001777; -;
 CC InterPro: IPR002465; -;
 CC Pfam: PF00041; fn3; 4.
 CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC
 CC SIGNAL 1 23 POTENTIAL.
 CC FT CHAIN 24 831 PROLACTIN RECEPTOR.
 CC FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 439 459 POTENTIAL.
 CC FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 123 225 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 228 325 FIBRONECTIN TYPE-III.
 CC FT DOMAIN 326 428 FIBRONECTIN TYPE-III.
 CC FT DISULFID 36 46 BY SIMILARITY.
 CC FT DISULFID 75 86 BY SIMILARITY.
 CC FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SEQUENCE 831 AA; 94394 MW; 220916320F7FAC1 CRC64;
 SQ
 Query Match 12.2%; Score 228; DB 1; Length 831;
 Best Local similarity 26.7%; Pred. No. 2.3e-11;
 Matches 91; Conservative 47; Mismatches 161; Indels 42; Gaps 15;
 QY 18 TTGCTGSSSDTEIKVN--PPQDFE--IVDPG-----YLGXYLQWQPLSL 59
 DB 97 TTNITVTATNETGSSSDPDYVDVTSIVGPGSVNITLETQRYANVILWAKWSPPLLA 156
 QY 60 DHPKECTVEYELKYRIGSTWTKTITIKNLHYKDGFDLNKGIEAKIHTLLPWOCTNGSEV 119


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FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 830 AA; 94507 MW; 38074E83CDF69EFF CRC64;

Query Match 11.28; Score 210.5; DB 1; Length 830;
Best Local Similarity 24.78; Pred. No. 6.4e-10;
Matches 86; Conservative 47; Mismatches 156; Indels 59; Gaps 14;

Qy 18 TFGCTSSDTEIKVNPQDFEIVDPGLG-----DPQVDVTSVQDPVNLSTETKTSASTYLLAKW 53
Db 97 TYINIVAMNEIGSNSS-----DPQVDVTSVQDPVNLSTETKTSASTYLLAKW 150

Qy 54 QPPLSLDFKECTV-EYELKYNIGSETWKTITKNLHYKDFGLNKIGIEAKIHTLLPWQ 112
Db 151 SPPLADVTSSHYRYELRLKPEKEWEIV---SVGVQYQKVNRLQAGVKYVQVR 206

Qy 113 CTNGSEVSSWAETTYTISPOG-IPETKVDQMDCCYVYNNQYLLCSWPKGIGVLLDTNYNL 171
Db 207 CVLDIGENSESSERHIIPNGESPPEKPTIIKCRSPKETFTCWKPKGSDGGHPTNTL 266

Qy 172 FYWEGDLHALQCVYDIKADQNGICRFPYLEADYKDFYICVNGSSSENKPIRSYFTFO 231
Db 267 LYSKEGEERVYCEPDY-KTAGPN-SCYFDKHTSFWTIYNTVATNIGSNVSDPLYVD 324

Qy 232 LQNIKVPPLPPVLTFTRESSCEIK----LKWS-IPLGPIPA-RCFDVEIEIREDDTLV 284
Db 325 VTYIVQTPPPNVNLELKKTVNRKPYLVLTWSPPLADVRSGWLTLDYELRLKPEEA--- 381

Qy 285 TATVENETTYTKTNETRQLCFV-----RSKNVNYCSDD--GIWSEWS 326
Db 382 -----EENETIFVGQOYHKFMSLNPGRKKYIVQIHKCPDHGHSNWS 424

RESULT 9
CYRG_HUMAN STANDARD; PRT; 369 AA.
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 30-JUL-1993 (Rel. 26, Last sequence update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-
DE 2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN).
GN IL2RG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=1631559;
RA Takeshita T., Asao H., Ohkani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor.";
RL Science 257:379-382(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93293887; PubMed=8514792;
RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;
RT "Characterization of the human interleukin-2 receptor gamma chain
RT gene";
RL J. Biol. Chem. 268:13601-13608(1993).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.

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RX MEDLINE=94004847; PubMed=8401490;
RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
RA Willard H., Henthorn P.S.;
RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
RL in X-linked severe combined immunodeficiency, SCIDX1.";
RN Hum. Mol. Genet. 2:1099-1104(1993).
RP [4]
RX IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090315; PubMed=8266076;
RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
RA Arai K.-I., Sugamura K.;
RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
RT receptors for IL-2 and IL-4.";
RL Science 262:1874-1877(1993).
RN [5]
RX IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090317; PubMed=8266078;
RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,
RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-4 receptor.";
RN Science 262:1880-1883(1993).
RP [6]
RX IDENTIFICATION AS A IL-7R SUBUNIT.
RX MEDLINE=94090316; PubMed=8266077;
RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-7 receptor.";
RN Science 262:1877-1880(1993).
RP [7]
RX 3D-STRUCTURE MODELING OF 57-248.
RX MEDLINE=95111953; PubMed=7529123;
RA Bamorough P., Hedecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
RL modelling.";
RN Structure 2:839-851(1994).
RP [8]
RX VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
RX MEDLINE=94130970; PubMed=8299698;
RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
RA de Saint Basile G.;
RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
RL severe combined immunodeficiency disease result in the loss of
RL high-affinity IL-2 receptor binding.";
RN Eur. J. Immunol. 24:475-479(1994).
RP [9]
RX VARIANT XSCID LYS-68.
RX MEDLINE=94375038; PubMed=8088810;
RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Detection of three nonsense mutations and one missense mutation in
RL the interleukin-2 receptor gamma chain gene in SCIDX1 that
RL differently affect the mRNA processing.";
RN Genomics 21:291-293(1994).
RP [10]
RX VARIANT XSCID HIS-162.
RX MEDLINE=94300093; PubMed=8027558;
RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
RT "Impairment of ligand binding and growth signaling of mutant IL-2
RL receptor gamma-chains in patients with X-linked severe combined
RL immunodeficiency.";
RN J. Immunol. 153:1310-1317(1994).
RP [11]
RX VARIANT XSCID ASN-39.
RX MEDLINE=95023932; PubMed=7937790;
RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Defective human interleukin 2 receptor gamma chain in an atypical X
RL chromosome-linked severe combined immunodeficiency with peripheral T
RL cells.";

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Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
[12]
VARIANTS XSCID CYS-226 AND HIS-226.
MEDLINE-9539784; PubMed=7668284;
RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
RT gene causing human X-linked severe combined immunodeficiency.";
RL Am. J. Hum. Genet. 57:564-571(1995).
[13]
VARIANT XSCID SER-183.
RP MEDLINE-96013903; PubMed=7557965;
RX Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
RA Levinsky R.L., Kinnon C.;
RT "Screening for mutations causing X-linked severe combined
RT immunodeficiency in the IL-2R gamma chain gene by single-strand
RT conformation polymorphism analysis.";
RL Hum. Genet. 96:427-432(1995).
[14]
VARIANT XSCID GLN-237 G-H-W INS.
RP MEDLINE-95164726; PubMed=7860773;
RX Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
RA "Female germ line mosaicism as the origin of a unique IL-2 receptor
RT gamma-chain mutation causing X-linked severe combined
RT immunodeficiency.";
RL J. Clin. Invest. 95:895-899(1995).
[15]
VARIANT XSCID GLN-271.
RP MEDLINE-95190013; PubMed=7883965;
RX Schmalstieg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E.,
RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
RT "Missense mutation in exon 7 of the common gamma chain gene causes a
RT moderate form of X-linked combined immunodeficiency.";
RL J. Clin. Invest. 95:1169-1173(1995).
[16]
VARIANT XSCID ARG-115.
RP MEDLINE-97042245; PubMed=8900089;
RX Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
RA Mueller-Fleckenstein I., Horneff G., Schrotten H., Fischer A.,
RA de Saint Basile G.;
RT "Atypical X-linked severe combined immunodeficiency due to possible
RT spontaneous reversion of the genetic defect in T cells.";
RL New Engl. J. Med. 335:1563-1567(1996).
[17]
VARIANT XSCID GLN-285.
RP MEDLINE-97295088; PubMed=9150740;
RX Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
RA Cant A., Kinnon C.;
RT "B-cell-negative severe combined immunodeficiency associated with a
RT common gamma chain mutation.";
RL Hum. Genet. 99:677-680(1997).
[18]
VARIANT XSCID CYS-222.
RX MEDLINE-98064061; PubMed=9399950;
RA Sharfe N., Shahar M., Roifman C.M.;
RT "An interleukin-2 receptor gamma chain mutation with normal thymus
RT morphology.";
RL J. Clin. Invest. 100:3036-3043(1997).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMAGLOBULINEMIA, SWISS TYPE
CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD132 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".
CC -!- DATABASE: NAME=IL2RGbase; NOTE=X-linked SCID mutation database;
CC WWW="http://www.nhgri.nih.gov/DIR/GMBS/SCID/".
CC
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DR EMBL; D11086; BAA01857.1; -
DR EMBL; L12183; AAA59145.1; -
DR EMBL; L12178; AAA59145.1; JOINED.
DR EMBL; L12176; AAA59145.1; JOINED.
DR EMBL; L12177; AAA59145.1; JOINED.
DR EMBL; L12179; AAA59145.1; JOINED.
DR EMBL; L12180; AAA59145.1; JOINED.
DR EMBL; L12181; AAA59145.1; JOINED.
DR EMBL; L12182; AAA59145.1; JOINED.
DR EMBL; L19546; AAC37524.1; -
DR PIR; A42565; A42565.
DR PDB; 1ILN; 26-JAN-95.
DR PDB; 1ILN; 26-JAN-95.
DR MIM; 308380; -
DR MIM; 300400; -
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
Query Match 10.8%; Score 202.5; DB 1; Length 369;
Best Local Similarity 24.8%; Pred. No. 1.1e-09;
Matches 61; Conservative 45; Mismatches 111; Indels 29; Gaps 9;
QY 97 LNKIEAKIHTLLPQCTNGSE-VQSSWAETTYWISPGIPETKVQDMDCVYNNQVLLC 155
DB 19 LGVGLNTILT-----PQNGEDTADFFLTMTDLSVSTLPLPEVQCFVFNVMNC 72
QY 156 SW-----KPGIGVLLDTNLYFYWEGLDH--ALQCVDIYIKADGONIGCRFPYLEASDY 207
DB 73 TWNSSEPPQ-----TNLTLYWYKNSDNDKVQKSHLYFSEITSGCLOKKEITHLY 125
QY 208 KDFVICYNGSSSEKPIRSSYFTFQLONTVLPVLYLTFTFRESSCEIKLWSIPLGPIPA 267
DB 126 QTFVYVQDPPRE--PRRQATQMLKQLNLVWPAPENLTLHLKLSQLELNNW---NRFNL 180
QY 268 RCFDYEIEIREDD-TTLVLTATVE-NETYYTLTKTNETQLCFVVRSKVNIYCSDDGIWSEW 325
DB 181 HCLEHLVQYRTDWDHSWTEQSDVYRHKFSLPSVDGQKRYTFRVRSRENPLCGSAQHSEW 240
QY 326 SDKOCW 331
DB 241 SHPIHW 246
RESULT 10
CYRG_CANFA
ID CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RX MEDLINE-95130114; PubMed=7829104;
RA Henthorn P.S., Somberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
RA Felsburg P.J.;
RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
RT severe combined immunodeficiency is a homologue of the human

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RT disease."
RL Genomics 23:69-74(1994).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; U04361; AAC48403.1; -.
DR HSSP; P31785; 1ILN.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 373 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 261 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 262 283 POTENTIAL.
FT DOMAIN 284 373 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 249 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089D8B CRC64;

Query Match 10.7%; Score 199.5; DB 1; Length 373;
Best Local Similarity 26.9%; Pred. No. 2e-09;
Matches 63; Conservative 40; Mismatches 96; Indels 35; Gaps 10;

Qy 115 NGSE-----VQSSWAETTYWISQGIPTKVDMDCVYNNWOYLCSW-----KPGI 161
Db 31 NGNEDITPDLTATPSET---LSVSLPLEVQ---CFVENVEYMNCTWNSSEPRP-- 82
Qy 162 GVLLTNNLFWYGL--DIALQCVDIKADQGNIGRFPYLEASDYKDFYCVNGSSE 219
Db 83 -----TSLTHWYKNSNDKVOEGCHGLFREVTAGCWLQKEETHLYETFFVQLDRPE 137
Qy 220 NKPIRSYFTQLONLVPLPPVLTFTRESSCEKLAWSIPLGPIPARCFDYEIEIRD 279
Db 138 --PRQSTQKLUKLQNLVLPWAPENLTNLNLSQLELSWS---NRHLDHCLVHVQVYRSD 192
Qy 280 -DTTLVATVEN-ETYLTKTNETRQLCFVVRKSKVNIYCSDDGIWSESDKQCW 331
Db 193 WDRSWTEQSDHRNSFSLPSVDGQGFYFRVRSRNYNPLCGSAQRWSEWSHPHW 246

RESULT 11
CYRG_MOUSE
ID CYRG_MOUSE STANDARD; PRT; 369 AA.
AC P34902.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors."
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma."
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RT Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RL chromosomal localization and expression in the adult thymus."
RN Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=B6.S;
RX MEDLINE=96341745; PubMed=8750189;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44."
RL J. Neurocol. 26:231-239(1995).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; D13821; BAA02974.1; -.
DR EMBL; U21795; AAA64279.1; -.
DR EMBL; D13565; BAA02760.1; -.
DR EMBL; L20048; AAA39286.1; -.
DR EMBL; S75852; AAB32904.1; -.
DR EMBL; S75844; AAB32904.1; JOINED.
DR EMBL; S75845; AAB32904.1; JOINED.
DR EMBL; S75847; AAB32904.1; JOINED.

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DR EMBL; S75848; AAB32904.1; JOINED.
DR EMBL; S75849; AAB32904.1; JOINED.
DR EMBL; S75850; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR EMBL; X75337; CRA53085.1; -.
DR PIR; JN0592; JN0592.
DR PIR; JN0775; JN0775.
DR HSSP; P31785; IILN.
DR MGD; MGI:96551; IL2I9.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 369
FT DOMAIN 23 263
FT TRANSMEM 264 369
FT DOMAIN 285 369
FT DOMAIN 151 250
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 71 71
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 96 96
FT CARBOHYD 159 159
FT CARBOHYD 164 164
SQ SEQUENCE 369 AA; 42241 MW; CB2DSAB459077AC7 CRC64;

Query Match 10.6%; Score 198.5; DB 1; Length 369;
Best Local Similarity 26.5%; Pred. No. 2.4e-09;
Matches 54; Conservative 38; Mismatches 95; Indels 17; Gaps 7;

QY 136 PETKYQDMDCVYNNQYLLCSW----KPGIGVLLDTNLYFWYBGLDHAL--QCVDYIK 189
Db 53 PTLPLPEQVCFENIEYNNCTWNSSEPQA-----TNLTLYRYKVSNDNTFQECSHYLF 107
QY 190 ADQGNIGCRFPYLEASDYKDFYICVNGSSSEKPIRSSYFTFQLOQNIYKPLPPVYLTFTRE 249
Db 108 SKEITSGCQIQKEDQLYQTFVQVL--QDPQKPRRAVQKLNQNLVTPRAPENLTLSNL 165
QY 250 SSECITKLKWSIPGLPIPARCFDYEIEIRD--DTTLVTATVENE--TYTLTKTTNETRQLCFV 307
Db 166 SESQLELRWK--SRHIKERCLOLYVOYRSNDRSRTWELIVNHEPRSLPSDELKRYTFR 223
QY 308 VRSKVNIYICSDGIIWSESDKQCV 331
Db 224 VRSRYNPICGSSQQSKWSQPVHW 247

RESULT 12
CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96268473; PubMed=9672241;
RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
```

```
gamma gene.*;
DNA Cell Biol. 15:453-459(1996).
-!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
INTERLEUKINS.
-!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
PROBABLY ALSO THE IL-13 RECEPTORS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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or send an email to license@isb-sib.ch).

EMBL; U33748; AAB07812.1; -.
HSSP; P31785; IILN.
InterPro; IPR000950; -.
InterPro; IPR001777; -.
InterPro; IPR002465; -.
Pfam; PF00041; fn3; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 379
FT DOMAIN 23 269
FT TRANSMEM 270 379
FT DOMAIN 291 379
FT DOMAIN 158 256
FT DISULFID 68 78
FT DISULFID 109 122
FT CARBOHYD 77 77
FT CARBOHYD 81 81
FT CARBOHYD 90 90
FT CARBOHYD 166 166
FT CARBOHYD 171 171
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.6%; Score 180; DB 1; Length 379;
Best Local Similarity 26.0%; Pred. No. 8.5e-08;
Matches 54; Conservative 38; Mismatches 90; Indels 26; Gaps 8;

QY 135 IPEKYQDMDCVYNNQYLLCSW-----KPGIGVLLDTNLYFWY---BGLDHALQCV 185
Db 61 LPLPKVQ---CFVFNVEYMNCTWNSSEPQP-----NNLTLYGYRNFGDDKLOECG 110
QY 186 DYKADGNIGCRFPYLEASDYKDFYICVNGSSSEKPIRSSYFTFQLOQNIYKPLPPVYLT 245
Db 111 HYLFSGITSGCWFQKKEIRLYETFFVQLODPREHR--KQPKMLKLDLVIPWAPENLT 168
QY 246 FTRESSCEIKLKWSIPGLPIPARCFDYEIEIRD--DTTLVTATVENE--ETYTLTKTTNETRQ 303
Db 169 LRNLSEFQLELSWS---NRYLDHCLHLYVOYRSNDRSRTWESQSVDRHSFSLPSVDAQKL 225
QY 304 LCFVVRSKVNIYICSDGIIWSESDKQCV 331
Db 226 YTFVRVSRYPNLCGSAQHWSDWSYPIHW 253

RESULT 13
IL3B_MOUSE
ID IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN PRECURSOR (COLONY
DE STIMULATING FACTOR 2 RECEPTOR, BETA 2 CHAIN).
GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
```


Qy 246 F-----TRESSCEIKLWSIP-LGPIPARCFDYEIEIREDTTLVTATVENETYTLKTTNE 300
Db 130 LEVKQLDKKTYLWVKWSPTITDVKTGFTMEYER-----LKPEAEWEIHFTH 182
Qy 301 TRQL-----CFVRSKVNICYSDDGWSEWSDKOCWE 332
Db 183 QTQFKVFDLYPGQKYLQTRCK---PDHGWSRWSQESSVE 220

Search completed: September 1, 2001, 19:16:27
Job time: 509 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:04 ; Search time 60.7 Seconds
(without alignments)
336.578 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLAIGCLYFLISTTF.....DDGIWSEWDKQWEGEDLS 337

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0601:*
- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
 - 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
 - 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
 - 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
 - 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
 - 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
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 - 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
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 - 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
 - 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
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 - 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
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 - 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
 - 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
 - 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
 - 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1873 | 100.0 | 380 | AAW24972 | Human interleukin- |
| 2 | 1873 | 100.0 | 380 | AAW35295 | Human IL-13 bindin |
| 3 | 1873 | 100.0 | 380 | AAW36613 | Human zcytor2 cyto |
| 4 | 1873 | 100.0 | 380 | AAW41520 | Human HR-1 recepto |
| 5 | 1873 | 100.0 | 380 | AAW41502 | Human cytokine/pep |
| 6 | 1873 | 100.0 | 380 | AAW33603 | Homo sapiens HR-1 |
| 7 | 1873 | 100.0 | 380 | AAV95296 | IL-13 binding chai |
| 8 | 1873 | 100.0 | 380 | AAV72136 | Human interleukin |
| 9 | 1873 | 100.0 | 380 | AAW22948 | Human IL-13 recept |
| 10 | 1847 | 98.6 | 380 | AAW36614 | Human zcytor2 cyto |
| 11 | 1725 | 92.1 | 315 | AAW56261 | Mature interleukin |

| | | | | | | |
|----|-------|------|------|----|----------|--------------------|
| 12 | 1725 | 92.1 | 359 | 19 | AAW56260 | Construct containi |
| 13 | 1718 | 91.7 | 372 | 18 | AAW36616 | Celebus macaque zc |
| 14 | 1184 | 63.2 | 383 | 18 | AAW35294 | Murine IL-13 bindi |
| 15 | 1184 | 63.2 | 383 | 21 | AAV95295 | IL-13 binding chai |
| 16 | 1184 | 63.2 | 383 | 22 | AAW72135 | Murine interleukin |
| 17 | 1184 | 63.2 | 383 | 22 | AAW29747 | Mouse IL-13 recept |
| 18 | 456 | 24.3 | 157 | 19 | AAW56252 | Interleukin-13 bin |
| 19 | 297 | 15.9 | 313 | 18 | AAW21856 | Protein used in pr |
| 20 | 293.5 | 15.7 | 396 | 13 | AAW22216 | Sequence of human |
| 21 | 293.5 | 15.7 | 396 | 13 | AAW22220 | Sequence of secret |
| 22 | 293.5 | 15.7 | 420 | 13 | AAW22219 | Human interleukin- |
| 23 | 293.5 | 15.7 | 420 | 19 | AAW82842 | Human IL-5 recepto |
| 24 | 292.5 | 15.6 | 421 | 13 | AAW25064 | Soluble human IL-5 |
| 25 | 292 | 15.6 | 335 | 13 | AAW25063 | shIL-5R-alpha. Sy |
| 26 | 292 | 15.6 | 335 | 14 | AAW33699 | IL5-R-GFP 130 fusi |
| 27 | 292 | 15.6 | 1026 | 16 | AAW70121 | Sequence of human |
| 28 | 288.5 | 15.4 | 420 | 13 | AAW22215 | Mouse interleukin- |
| 29 | 287.5 | 15.3 | 426 | 18 | AAW09821 | Human interleukin- |
| 30 | 285 | 15.2 | 427 | 18 | AAW24973 | Human interleukin- |
| 31 | 285 | 15.2 | 427 | 22 | AAW19807 | IL-13/IL-4 dual tr |
| 32 | 285 | 15.2 | 793 | 21 | AAW92208 | Human interleukin- |
| 33 | 284 | 15.2 | 426 | 18 | AAW09822 | IL-13/IL-4 dual tr |
| 34 | 284 | 15.2 | 784 | 21 | AAW92207 | Human interleukin- |
| 35 | 283 | 15.1 | 427 | 22 | AAW19808 | IL-13/IL-4 dual tr |
| 36 | 230 | 12.3 | 398 | 13 | AAW22212 | Sequence of interl |
| 37 | 229 | 12.2 | 315 | 13 | AAW22214 | Sequence of interl |
| 38 | 229 | 12.2 | 332 | 13 | AAW22213 | Sequence of interl |
| 39 | 229 | 12.2 | 332 | 13 | AAW22218 | Sequence of interl |
| 40 | 229 | 12.2 | 415 | 13 | AAW22211 | Sequence of interl |
| 41 | 229 | 12.2 | 415 | 13 | AAW22217 | IL-2 receptor gamm |
| 42 | 202.5 | 10.8 | 252 | 15 | AAW47150 | IL-2 receptor gamm |
| 43 | 202.5 | 10.8 | 369 | 15 | AAW47148 | Human cytokine rec |
| 44 | 202.5 | 10.8 | 482 | 19 | AAW31646 | Fusion polypeptide |
| 45 | 202.5 | 10.8 | 691 | 21 | AAW92202 | |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| AAW24972 | AAW24972 standard; protein; 380 AA. |
| ID | AC |
| XX | AAW24972; |
| XX | 22-JUN-1998 (first entry) |
| DT | Human interleukin-13 beta receptor. |
| DE | Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13. |
| XX | Homo sapiens. |
| OS | WO9720926-A1. |
| PN | 12-JUN-1997. |
| XX | 07-NOV-1996; 96WO-FR01756. |
| XX | 06-DEC-1995; 95FR-0014424. |
| PR | (SNFI) SANOFI SA. |
| PA | Caput D, Ferrara P, Laurent P, Vita N; |
| XX | WPI; 1997-319773/29. |
| XX | N-PSDB; AAT85826, AAT86464. |
| XX | New purified human interleukin-13 receptors - and related nucleic |
| PT | acids, useful for diagnosis and treatment of inflammation, allergy, |
| PT | etc |
| XX | Claim 1; Figure 2a; 83pp; French. |
| PS | |

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are designated for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunoassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCGLYFLISTTFTGCTSSDTEIKVNPQQDFEIVDPGVLGYLYLQWQPPLSLD 60
 DB 1 mafvclaigcglyflisttftgctssdteikvnpqqdfelvdpvglylylqwqpplsl 60
 QY 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKEAKIHLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktitknlykdgfdlنگkeakihllpwqctngsevg 120
 QY 121 SSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSKPKGVLGVDNLYNLFYWEGLDH 180
 DB 121 sswaettywispgipetkvdmdcvynnwqyllcswkpgvgldntnlyfweyegldh 180
 QY 181 ALQCVDIYKADQGNIGCRFFYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
 DB 181 alqcvdyikadgnigcrffyleasdykdfyicvngssenkprrsyftfolqnvkplp 240
 QY 241 PVIYLTFTRESSECEIKLWSIPGLPIPARCFDYEIREDDTTLVTAVENETYTLKTTNE 300
 DB 241 pviyftftressceiklwsipglpmparcfdyeirreddttlvatvenetytlktne 300
 QY 301 TROLCFVVRKVNLYCSDGGLWSWSKQCEGEDLS 337
 DB 301 trqlcfvvrskvnlycsddglwswskqcegedls 337

RESULT 2

ID AAW35295 standard; Protein; 380 AA.

XX AAW35295;

XX 27-MAR-1998 (first entry)

XX Human IL-13 binding chain of the IL-13 receptor.

XX Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT /label= signal_sequence
 FT /note= "putative"
 FT 26..380
 FT /label= mature_protein
 FT 26..341
 FT /label= extracellular_domain
 FT 342..362
 FT /label= transmembrane_domain
 FT 363..380
 FT /label= intracellular_domain

XX W09731946-A1.

PN 04-SEP-1997.

XX 28-FEB-1997; 97WO-US03124.

PR 01-MAR-1996; 96US-0609572.

PA (GEMY) GENETICS INST INC.

PI Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;

XX WPI; 1997-448632/41.

DR N-PSDB; AAT95214.

XX New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis

XX Claim 11; Pages 34-35; 49pp; English.

XX The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCGLYFLISTTFTGCTSSDTEIKVNPQQDFEIVDPGVLGYLYLQWQPPLSLD 60

DB 1 mafvclaigcglyflisttftgctssdteikvnpqqdfelvdpvglylylqwqpplsl 60

QY 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKEAKIHLLPWQCTNGSEVQ 120

DB 61 hfkectveyelkynigsetwktitknlykdgfdlنگkeakihllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSKPKGVLGVDNLYNLFYWEGLDH 180

DB 121 sswaettywispgipetkvdmdcvynnwqyllcswkpgvgldntnlyfweyegldh 180

QY 181 ALQCVDIYKADQGNIGCRFFYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240

DB 181 alqcvdyikadgnigcrffyleasdykdfyicvngssenkprrsyftfolqnvkplp 240

QY 241 PVLFTRESSCEIKLWSIPIGPIPARCFDYEIEIREDDTTLVATVENETYLTKTNE 300
Db 241 pvlftressceiklwsipigpiparcfdyeiieireddttlvatvenetytlktne 300
QY 301 TROLCFVVRKSNVNYCSDGWIWSEWSDKQWGEDLS 337
Db 301 trqlcfvvrksnvnycsddgiwsewsdkqwegeds 337

RESULT 3

AAW36613

ID AAW36613 standard; Protein; 380 AA.

XX

AC AAW36613;

XX

DT 30-MAR-1998 (first entry)

XX

DE Human Zcytor2 cytokine receptor protein.

XX

KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain

FT 340..363

FT /label= transmembrane_domain

FT Domain

FT 364..380

FT /label= intracellular_domain

FT Domain

FT 25..339

FT /label= ligand_binding_domain

XX

PN WO9733913-A1.

XX

PD 18-SEP-1997.

XX

PF 12-MAR-1997; 97WO-US04043.

XX

PR 13-MAR-1996; 96US-0013345.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;

XX

PI O'Hara PJ;

XX

DR WPI; 1997-470820/43.

XX

DR N-PSDB; AAT96782.

XX

XX New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment

XX

XX Claim 2; Page 47-48; 79pp; English.

PS

CC This sequence represents a novel ligand-binding receptor, zcytor2,
CC which shares homology with cytokine receptors and was isolated from human
CC placental polyA+ RNA. The resulting polypeptide is a receptor for
CC cytokines (particularly interleukin-13) and is expressed on the surface
CC of testicular cells, probably being involved in spermatogenesis. It can
CC be used to detect ligands that promote proliferation and/or
CC differentiation of such cells in cultures and may also be used to treat
CC infertility. Antagonists of this receptor may be used to characterise
CC ligand-receptor interactions and as male-specific contraceptives. By
CC blocking the action of IL-13, receptor antagonists and ligand-binding
CC this receptor can also be used to modulate immune function, e.g. in
CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.

XX Sequence 380 AA;

SQ

Query Match 100.0%; Score 1873; DB 18; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.6e-176;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTFGCTSSDTEIKVNPQDDEIVDPGVLGYLQWQPPLSLD 60

Db 1 mafvclaigclytflistfgctssdteikvnpqdfvdpvgylglwqpplslid 60

QY 61 HFKECTVEVELKYRNISETWKTIIITKNLHYKDGFDLANKIEAKIHTLLPWQCTNGSEVO 120

Db 61 hfkectveyelkyrni9setwktiiitknlhykdgfdlnk9ieakihltlpwqctngsevq 120

QY 121 SSWAETTYWISPOGIPETKVDMDCVYINWQYLLGSWRPGIGVLDTNINLFYWTYEGLDH 180

Db 121 sswaettywispogipetkvdmdcvynwqyllcswrpgigvlltdntynlffwyegldh 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQLOIVKPLP 240

Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkprrssytfqlnivkplp 240

QY 241 PVLFTRESSCEIKLWSIPIGPIPARCFDYEIEIREDDTTLVATVENETYLTKTNE 300

Db 241 pvlftressceiklwsipigpiparcfdyeiieireddttlvatvenetytlktne 300

QY 301 TROLCFVVRKSNVNYCSDGWIWSEWSDKQWGEDLS 337

Db 301 trqlcfvvrksnvnycsddgiwsewsdkqwegeds 337

RESULT 4

AAW41520

ID AAW41520 standard; Protein; 380 AA.

XX

AC AAW41520;

XX

DT 22-JUN-1998 (first entry)

XX

DE Human HR-1 receptor.

XX

KW HR-1 receptor; human; cytokine; infection; asthma; allergy;

XX

KW haematopoietic disorder; tumour; therapy; diagnosis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide

FT 1..21

FT /label= Sig_peptide

FT Protein

FT 22..380

XX /label= Mat_protein

XX

PN WO9747741-A1.

XX

PD 18-DEC-1997.

XX

PF 12-JUN-1996; 96WO-US10262.

XX

PR 12-JUN-1996; 96WO-US10262.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Appelbaum ER, Hu J;

XX

DR WPI; 1998-052308/05.

XX

DR N-PSDB; AAW04131.

XX

PT Nucleic acid sequence encoding human cytokine peptide hormone

XX

PT receptor - useful to treat, prevent or diagnose, e.g. lowered

XX

PS resistance to infection, asthma, allergy or haematopoietic disease

XX

XX Claim 13; Page 62-64; 76pp; English.

CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated the HR-1 receptor, that shows 27% identity
 CC and 52% similarity to the interleukin-5 receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
 CC human testis library. Recombinant HR-1 receptor can be expressed
 CC in claimed host cells, and used in a claimed method for identifying
 CC compounds which bind to, and activate or inhibit, it. HR-1
 CC receptor activators and agonists can be used to treat, prevent or
 CC diagnose predisposition to lowered resistance to infection, asthma,
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
 CC be used to treat conditions associated with HR-1 receptor
 CC overexpression. The antibodies can also be used to determine HR-1
 CC receptor levels, since overexpression may be diagnostic of tumours.

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTGCTSSDTEIKVNPDPDFEIVDPGVLGYLYLQWQPPPLSLD 60
 DB 1 mafvclaigcltyflstftgctssdteikvnpdpdfeivdpgylgylylqwppplsl 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynrigsetwktititknhykdgfdlnkgeakihllpwqctngsevg 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSKPKGIGVLLDTNLYNFYWEGLDH 180
 DB 121 sswaettywispqgipetkvqdmcdvynnwqyllcswkpgigvlltdtnnlyfywegl 180
 QY 181 ALQCVDYIKADQNGICGRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadgngicgrfyleasdykdfyicvngsssenkpirssyftfqlqivkplp 240
 QY 241 PVLTLFTRESSECEIKLWSIPGLPIPARCFDYEIEIREDDTLVTATVENETYTLTKTNE 300
 DB 241 pylvltftressceiklwsipglpiparcfdyeieireddtlvtatvenetytlktne 300
 QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLS 337
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqcegedls 337

RESULT 5
 ID AAW41502
 XX AAW41502 standard; Protein; 380 AA.

AC AAW41502;

DT 08-JUN-1998 (first entry)

XX Human cytokine/peptide receptor, HR-1 receptor.

DE HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
 KW neutropaenia; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT Protein 22..380
 FT /label= Mat_protein
 FT /note= "Claim 14"

XX EP812913-A2.

XX

PD 17-DEC-1997.
 XX 04-JUN-1997; 97EP-0303815.
 XX 12-JUN-1996; 96US-0017843.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX Appelbaum ER, Hu J;
 XX WPI; 1998-034974/04.
 DR N-PSDB; AAV04075.
 XX Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 XX
 PS Claim 13; Page 27-28; 34pp; English.

CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor. The amino acid sequence
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human
 CC testis cDNA library. It shows 27% amino acid identity and 52%
 CC similarity with the human interleukin-5 receptor. Also claimed are
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an
 CC agonist to the polypeptide, antibody against the polypeptide, an
 CC antagonist that inhibits the activity of the polypeptide, a process
 CC for diagnosing a disease, or a susceptibility to disease, related
 CC to expression of HR-1 receptor, and a method for identifying
 CC compounds that activate or inhibit the HR-1 receptor. HR-1
 CC receptor protein and polynucleotides can be used for research,
 CC biological, diagnosis and (gene) therapy applications, e.g. to
 CC increase resistance to infections in individuals with trauma and/or
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropaenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTGCTSSDTEIKVNPDPDFEIVDPGVLGYLYLQWQPPPLSLD 60
 DB 1 mafvclaigcltyflstftgctssdteikvnpdpdfeivdpgylgylylqwppplsl 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynrigsetwktititknhykdgfdlnkgeakihllpwqctngsevg 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSKPKGIGVLLDTNLYNFYWEGLDH 180
 DB 121 sswaettywispqgipetkvqdmcdvynnwqyllcswkpgigvlltdtnnlyfywegl 180
 QY 181 ALQCVDYIKADQNGICGRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadgngicgrfyleasdykdfyicvngsssenkpirssyftfqlqivkplp 240
 QY 241 PVLTLFTRESSECEIKLWSIPGLPIPARCFDYEIEIREDDTLVTATVENETYTLTKTNE 300
 DB 241 pylvltftressceiklwsipglpiparcfdyeieireddtlvtatvenetytlktne 300
 QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLS 337
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqcegedls 337

RESULT 6

AAW33603
ID AAW33603 standard; Protein; 380 AA.

AC AAW33603;

DT 08-JUN-1998 (first entry)

XX Homo sapiens HR-1 receptor.

XX Cytokine; hormone receptor; AIDS; acquired immune deficiency;
syndrome; aplastic anaemia; neutropaenia; cancer treatment;
infection resistance; diagnosis; tumours; HR-1 receptor;
XX asthma; allergic; haematopoietic; disorder.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Peptide 1..21
/note= "signal peptide"

XX W09747742-A1.

XX 18-DEC-1997.

XX 09-JUL-1996; 96WO-US11459.

XX 12-JUN-1996; 96WO-US10262.

XX 12-JUN-1996; 96US-0017843.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Appelbaum ER, Hu J;

XX WPI; 1998-052309/05.

XX N-PSDB; AAV02295.

XX DNA encoding human cytokine-peptide hormone receptor - useful for
treating preventing or diagnosing, e.g. lowered resistance to
infection, asthma, allergy, or haematopoietic disease

XX Claim 15; Fig 1; 75pp; English.

XX The sequence is that of the human cytokine/peptide hormone receptor
(HR-1 receptor). This, or it's activators or agonists, can be used to
treat, prevent or diagnose predisposition to lowered resistance to
infection, asthma, allergic or haematopoietic disorders, e.g. where
induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
neutropaenia or cytotoxic treatments for cancer. Antagonists of the
receptor, e.g. antibodies or fragments of it may be used to treat
conditions associated with overexpression of the HR-1 receptor, e.g.
those listed above. Antibodies may also be used to assay levels of HR-1
receptor, overexpression of which may be diagnostic of tumours, by usual
immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
for affinity purification of the HR-1 receptor.

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.6e-176;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAGLCYTLTFTGCTSSSTDEIKVNPQDFEIVDPGLGLYLQWPPPLSLD 60

Db 1 mafvclaglcyltltftgctssstdeikvnpqdfelvdpqglgllylqwpplsl 60

QY 61 HFKECTVEYELKYNIGSETWKTITITNLHYKDGFDLNGKTEAKHTLLPQCTNGSEVQ 120

Db 61 hfkectveyelkynigsetwktititnlhykdgfdlنگkتهاکهتllpqctngse 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180

XX

Db 121 sswaettywispggipetkvdmdcvynwqyllicswkpgigvlltdnynlfywegldh 180
XX
QY 181 ALCQVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNLVKPLP 240
XX
Db 181 alqcvdyikadgngicrfpyleasdykdfyicvngssenkpirssyftfqlqnlvkplp 240
XX
QY 241 PVIYLTFTRESSCEIKLKWSPGLPGIPARCFDYEIEIREDDTTLVTATVENEYTLTKTNE 300
XX
Db 241 pviyftressceiklkwspglpkiparcfdyeieireddttltvtatvenetytlktne 300
XX
QY 301 TRQICFVVRKVNICYSDDGIIWSEWSKQWEGEDLS 337
XX
Db 301 trqicfvvrskvniycsddgiwsewskqcgwedls 337
XX

RESULT 7

AA95296

ID AAY95296 standard; Protein; 380 AA.

XX AAY95296;

XX 12-SEP-2000 (first entry)

XX IL-13 binding chain of human IL-13 receptor.

XX Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
immune complex disease; lupus; nephritis; thyroiditis;
XX Grave's disease; inflammatory; infection; therapy; antiallergic;
antiinflammatory; antiasthmatic; vaccine.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Peptide 1..25
/note= "signal peptide"

FT Protein 26..380
/note= "mature protein"

FT Domain 26..341
/note= "extracellular domain; a polypeptide

FT comprising amino acids 22-334 is
specifically claimed in Claim 11(e)"
Domain 342..362
/note= "transmembrane domain"

FT Domain 363..380
/note= "intracellular domain; a polypeptide

FT comprising amino acids 257-383 is
specifically claimed in Claim 11(f)"
XX WO200036103-A1.

XX 22-JUN-2000.

XX 13-DEC-1999; 99WO-US29493.

XX 14-DEC-1998; 98US-0211335.

XX (GEMY) GENETICS INST INC.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;

XX Wills-Karp M;

XX WPI; 2000-431587/37.

XX N-PSDB; AAA27912.

XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of

an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
asthma, Grave's disease and inflammatory conditions of the lung -

XX Claim 11(d); Page 53-54; 60pp; English.

XX The present sequence is that of the interleukin-13 binding chain

XX

(IL-13bc) of the human IL-13 receptor, as deduced from an isolated human testis cDNA clone (see AAA27912). IL-13bc is a member of the haematopoietin receptor family that acts as a mediator of IL-13. The invention provides methods for the recombinant production of IL-13bc polypeptides, including claimed full-length IL-13bc, its extracellular domain, and its intracellular domain. IL-13bc polypeptides, particularly soluble IL-13bc polypeptides, and IL-13 receptor inhibitors (e.g. antagonists of the interaction of IL-13 and its receptor) can be used to treat conditions in which IL-13 is implicated, particularly IgE-mediated conditions and diseases including atopy, allergy, asthma, immune complex diseases (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis, thyroiditis and Grave's disease), lung inflammation, immunodeficiency, and cancer. Since IL-13 inhibits macrophage activation, IL-13bc proteins can also be used to enhance macrophage activation, e.g. in vaccination, treatment of mycobacterial or intracellular organisms or parasite infections. IL-13bc proteins may also be used to potentiate the effects of IL-13 in vitro and in vivo, as diagnostic agents, and to screen for agents capable of binding to IL-13bc or IL-13 receptor, or which interfere with the binding of IL-13 to its receptor.

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 21; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIAGCLYTLFTTFCGTSSTDEIKVNPQDFEIVDPGVLYLQWQPPPLSLD 60
 Db 1 mafvclaigcltyflsttfgctssdteikvnpqdfvdpvglylylqwgpplsld 60

QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLANKGIEAKHTLLPWCQTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlhykdgfdlnkgieakhtllpwqctngsevq 120

QY 121 SSWAETTWISPGQIPETKVDMDCVYNNWQVLLCSWPKPGIGVLDITNLYFYWYEGLDH 180
 Db 121 sswaettwispgqipetkvdmdcvynnwqyllcswpkpgigvlditnlyfywyegldh 180

QY 181 ALQCVDYIKAGQNTGCRPPYLEADYKDFYICVNGSENKPIRSSYTFQLONTKPLP 240
 Db 181 alqcvdyikadqngicrfyleadykdfyicvngsenkpirssytfqlqnlvklp 240

QY 241 PVLFTFRESSCEIKLWSIPGPAPARCFDYEIFREDDTLVTATVENETYTKTTNE 300
 Db 241 pvlftfressceiklwsipgparcfdyeyefreddtlvtatvenetytkttne 300

QY 301 TRQLCFVVRKSNVYICSDDGWSEWSRQCWGEDLS 337
 Db 301 trqlcfvvrksnvycsddgiwsewsdkqcwgedls 337

RESULT 8
 AAY72136
 ID AAY72136 standard; Protein; 380 AA.
 AC AAY72136;
 XX
 XX 24-APR-2001 (first entry)
 DE Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
 KW Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
 KW therapy; tissue fibrosis; Schistosoma infection; surgical incision;
 KW cytostatic; wound; IL-13 related condition; allergic condition;
 KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
 KW macrophage activation.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers

Peptide 1..25
 /label= Signal_peptide
 FT Region 1..81
 /note= "This region is identical to the translated
 FT sequence of an expressed sequence tag (EST) identified
 FT as yg99f10.r1 human cDNA clone 41648 5"
 FT 26..380
 /label= Mature_human_interleukin (IL)-13_binding_chain_
 FT of_IL-13_receptor
 FT 26..341
 /note= "Extracellular domain; this region is specifically
 FT claimed in claims 1e, 6e, 15e and 23e"
 FT 342..362
 /note= "Transmembrane domain"
 FT 363..380
 /note= "Intracellular domain; this region is specifically
 FT claimed in claims 1f, 6f, 15f and 23f"
 XX
 PN WO200078336-A1.
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-US17103.
 PF
 XX 21-JUN-1999; 99US-0334512.
 PR
 XX (GEMY) GENETICS INST INC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 PI Wills-Karp M;
 PI
 XX WPI: -2001-080753/09.
 DR N-PSDB: AAD02335.
 XX
 PT Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
 PT in a mammalian subject, involves administering a pharmaceutical
 PT composition comprising IL-13 antagonist -
 XX
 PS Claim 1a; Page 69-70; 72pp; English.
 XX
 CC The invention relates to a method of treating, or inhibiting
 CC the formation of tissue fibrosis in mammals, which involves
 CC administering a pharmaceutical composition comprising interleukin
 CC (IL)-13 antagonist. The protein of the invention is useful for
 CC treating tissue fibrosis resulting from infection with Schistosoma
 CC or from healing of a wound which is a surgical incision, or
 CC inhibiting formation of tissue fibrosis which affects tissues such
 CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 CC biliary tract and gut. It is also used in the treatment or modulation
 CC of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
 CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIAGCLYTLFTTFCGTSSTDEIKVNPQDFEIVDPGVLYLQWQPPPLSLD 60
 Db 1 mafvclaigcltyflsttfgctssdteikvnpqdfvdpvglylylqwgpplsld 60

QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLANKGIEAKHTLLPWCQTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlhykdgfdlnkgieakhtllpwqctngsevq 120

Db 61 hflectveyelkynrigsetwktiitknlhykdgfdlnkgleakihltlpwqctngseq 120
Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWOYLLCSWPKGVLDDTNNFLFYWEGLDH 180
Db 121 sswaettywispqgipetkvdmdcvynnywqyllycswwpvgvldtdnnyfyywvgeidh 180
Qy 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqonigcrfpyleasydkdfyicvngsssenkpirssyftfqlqnvkplp 240
Qy 241 PVYLTFTRESSCEIKLWSIPLGPPIPARCFDYEIEIREDDTTLVTATVENETYTLTKTNE 300
Db 241 pvytlftressceiklwsiplgpiparcfdyeieireddttltvtatvenetytlktne 300
Qy 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEDLS 337
Db 301 trqlcfvvrskvnicycsddgiwsewsdkqcegedls 337
RESULT 9
ID AAB29748 standard; Protein; 380 AA.
AC AAB29748;
XX
XX 23-FEB-2001 (first entry)
XX Human IL-13 receptor IL-13 binding chain (IL-13bc).
XX Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulneryary;
KW wound healing; schistosoma infection; liver; skin; muscle;
KW cartilage; cardiac tissue; lung tissue; uterine tissue;
KW intestinal tissue; vascular tissue; neural tissue.
XX Homo sapiens.
XX WO200064944-A1.
XX 02-NOV-2000.
XX 28-APR-2000; 2000WO-US11612.
XX 28-APR-1999; 99US-0301808.
XX (GEMY) GENETICS INST INC.
XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
PI Whitters MJ, Wood C;
XX WPI; 2001-024676/03.
XX N-PSDB; AAC81416.
XX Treating or inhibiting tissue fibrosis resulting from infection with
PT schistosoma and wound healing involves administering interleukin-13 or
PT interleukin-4 antagonist -
XX Claim 1; Page 76-77; 82pp; English.
XX The invention relates to a method of treating fibrosis in a mammal
CC by administering an interleukin-13 (IL-13) antagonist or an IL-4
CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding
CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or
CC soluble fragments thereof. The method is useful for treating or
CC inhibiting the formation of tissue fibrosis resulting from the healing
CC of a wound, including a surgical incision wound, or from infection with
CC schistosoma. The method may be used to treat fibrosis in a variety of
CC tissues, particularly liver tissue, but also skin epidermis, skin
CC endoderms, muscle, tendon, cartilage, cardiac tissue, pancreatic
CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,
CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
CC tissue. The present sequence represents human IL-13bc.
XX

SQ Sequence 380 AA;
Query Match 100.0%; Score 1873; DB 22; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.6e-176;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIGCLYTLFLISTFGCTSSSDTEIKVNPQDFEIVDPDGYLVLYLQWQPPPLSLD 60
Db 1 mafvclaigcllytlflistfgctsssdteikvnpqdfeiavdpdgylylylqwpplslid 60
Qy 61 HFKECTVEYELKYRNIGSETWKTITKLNHYKDGFDLNKGLEAKIHITLLPWQCTNGSEVQ 120
Db 61 hflectveyelkynrigsetwktiitknlhykdgfdlnkgleakihltlpwqctngseq 120
Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWOYLLCSWPKGVLDDTNNFLFYWEGLDH 180
Db 121 sswaettywispqgipetkvdmdcvynnywqyllycswwpvgvldtdnnyfyywvgeidh 180
Qy 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqonigcrfpyleasydkdfyicvngsssenkpirssyftfqlqnvkplp 240
Qy 241 PVYLTFTRESSCEIKLWSIPLGPPIPARCFDYEIEIREDDTTLVTATVENETYTLTKTNE 300
Db 241 pvytlftressceiklwsiplgpiparcfdyeieireddttltvtatvenetytlktne 300
Qy 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEDLS 337
Db 301 trqlcfvvrskvnicycsddgiwsewsdkqcegedls 337
RESULT 10
ID AAW36614 standard; Protein; 380 AA.
XX
XX AAW36614;
XX 30-MAR-1998 (first entry)
XX Human Zcytor2 cytokine receptor protein.
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX Homo sapiens.
XX WO9733913-A1.
XX 18-SEP-1997.
XX 12-MAR-1997; 97WO-US04043.
XX 13-MAR-1996; 96US-0013345.
XX (ZYMO) ZYMOGENETICS INC.
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'Hara PJ;
XX WPI; 1997-470820/43.
XX N-PSDB; AAT96783.
XX New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX Claim 1; Page 51-53; 79pp; English.
XX This sequence represents a novel ligand-binding receptor, Zcytor2, which
CC shares homology with cytokine receptors and was isolated from a human
CC testis cDNA library. The resulting polypeptide is a receptor for
CC cytokines (particularly interleukin-13) and is expressed on the surface

of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as antagonist.

Sequence 380 AA;

Query Match 98.6%; Score 1847; DB 18; Length 380;
Best Local Similarity 99.1%; Pred. No. 2.4e-173;
Matches 334; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTFGCTSSDTEIKVNPDPDFEIVDPGVLGYLYLQWQPPLSLD 60
DB 1 mafvclaigcltytlstfgctssdteikvnpdpdfEIVDPGVLGYLYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
DB 61 hfkeytveyelkynigsetwktitknlhykdgfdlnkgeakihltllpwqctngseVq 120
QY 121 SSWAETTWISPOGIPETKVDQMCVYVNWQYLLCSWPKGIGVLLDTNLYNLFYWEGLDH 180
DB 121 sswaettwispgipetkvgdmdcvyynwqyllcsWPKGIGVLLDTNLYNLFYWEGLDl 180
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFOLQNVKPLP 240
DB 181 alqcvdyikadgqnlgcrfpyleasdykdfyicvngssenKPIRSSYTFqlqnvkPlp 240
QY 241 PYYLFTRESSCEIKLWSIPLGPAPRCFDYIEIREDDTTLVTATVENETYTLTKTNE 300
DB 241 pylvltfressceiklwgiplgpIparcfdyeiEireddtllvtatvenetytlktne 300
QY 301 TRQLCFVVRKVNIIYCSDDGIWSEWSKQCEGEDLS 337
DB 301 trqlcfvvrskvniycsddgiwsewsdkqcwgedls 337

RESULT 11
AAW56261
ID AAW56261 standard; Protein; 315 AA.

AC AAW56261;

DT 16-SEP-1998 (first entry)

XX Mature interleukin-13 binding protein.

DE Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.

XX Homo sapiens.

XX WO9810638-A1.

XX 19-MAR-1998.

XX 10-SEP-1997; 97WO-AU00591.

XX 27-FEB-1997; 97AU-0005374.

XX 10-SEP-1996; 96AU-0002262.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;

XX

DR WPI; 1998-207062/18.
DR N-PSDB; AAV22702.

PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection

XX Disclosure; Page 55-56; 69pp; English.

XX The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.

XX Sequence 315 AA;

Query Match 92.1%; Score 1725; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPPODFEIVDPGVLGYLYLQWQPPLSLDHFKECTVEYELKYNIGSETWKTITKN 88
DB 1 eikvnpdpdfEIVDPGVLGYLYLQWQPPLSLDHFKECTVEYELKYNIGsetwktitkn 60

QY 89 LHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQSSWAETTYWISPOGIPETKVDQMCVY 148
DB 1 hykdgfdlnkgeakihltllpwqctngsevqsswaettywispqIpetkvqmdcvyy 120

QY 149 NWQYLLCSWPKGIGVLLDTNLYNLFYWEGLDHALQCVDYIKADGONIGCRFPYLEASDYK 208
DB 121 nwqyllcsWPKGIGVllDtnnlfyWegldhAlqcvdyikadgqnlgcrfpyleasdyk 180

QY 209 DFYICVNGSSSENKPIRSSYTFOLQNVKPLPPVYLTFTRESSCEIKLWSIPLGPAP 268
DB 181 dfyicvngssenKPIRSSYTFqlqnvkPlppvyltftressceiklwsipIgpap 240

QY 269 CFDEIEIREDDTTLVTATVENETYTLTKTNETROLQCFVVRKVNIIYCSDDGIWSEWSK 328
DB 241 cfdyeieireddtllvtatvenetytlktNetrqlcfvvrskvniycsddgiwsewsdk 300

QY 329 QCWEGEDLS 337
DB 301 qcwgedls 309

RESULT 12

AAW56260

ID AAW56260 standard; Protein; 359 AA.

XX AAW56260;

DT 16-SEP-1998 (first entry)

DE Construct containing mature interleukin-13 binding protein.

XX Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.

XX Homo sapiens.

XX WO9810638-A1.

XX 19-MAR-1998.

XX 10-SEP-1997; 97WO-AU00591.

XX 27-FEB-1997; 97AU-0005374.

XX 10-SEP-1996; 96AU-0002262.

XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX WPI; 1998-207062/18.
DR N-PSDB; AAV22701.
XX New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX Example 14; Page 52-53; 69pp; English.
XX The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX Sequence 359 AA;
XX
XX Query Match 92.1%; Score 1725; DB 19; Length 359;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-161;
XX Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 EIKVNPDDFEIVDPGILGYLQWQPLSLDHFKECVNELKYNIGSETWKIIITKN 88
Db 45 EIKVNPDDFEIVDPGILGYLQWQPLSLDHFKECVNELKYNIGSETWKIIITKN 104
Qy 89 LHYKDGFDLNGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVY 148
Db 105 LHYKDGFDLNGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVY 164
Qy 149 NNQYLLCSWKPGIGVLLDTNVLNFWYBGLDHALQCVYIKADGONIGCRFPYLEADYK 208
Db 165 NNQYLLCSWKPGIGVLLDTNVLNFWYBGLDHALQCVYIKADGONIGCRFPYLEADYK 224
Qy 209 DFYICVNGSSENKPIRSSVFTFOLNIVKPLPPVLTFTRESSCEIKLWSIPGLPIPAR 268
Db 225 DFYICVNGSSENKPIRSSVFTFOLNIVKPLPPVLTFTRESSCEIKLWSIPGLPIPAR 284
Qy 269 CPDYIEIREDDTLTIVATVENETTLKTTNETRQLCFVRSKVNICYSDGCIWSEWSDK 328
Db 285 CPDYIEIREDDTLTIVATVENETTLKTTNETRQLCFVRSKVNICYSDGCIWSEWSDK 344
Qy 329 QCWEGEDLS 337
Db 345 QCWEGEDLS 353
RESULT 13
AAW36616
ID AAW36616 standard; Protein; 372 AA.
XX
XX AAW36616;
XX
XX 30-MAR-1998 (first entry)
XX Celebus macaque zcytor2 protein.
XX
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX
XX Macaque sp.
XX
XX Key Location/Qualifiers
XX Protein 1..372
XX /label= zcytor2
XX /note= "partial protein sequence"
XX

PN WO9733913-A1.
XX 18-SEP-1997.
XX 12-MAR-1997; 97WO-US04043.
XX 13-MAR-1996; 96US-0013345.
XX (ZYMO) ZYMOGENETICS INC.
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'Hara PJ;
XX WPI; 1997-470820/43.
DR N-PSDB; AAT96784.
XX New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX Example 4; Page 56-57; 79pp; English.
XX This sequence represents a novel ligand-binding receptor, Zcytor2,
CC which shares homology with cytokine receptors and is isolated from
CC testis tissue obtained from a Celebus macaque. The resulting polypeptide
CC is a receptor for cytokines (particularly interleukin-13) and is
CC expressed on the surface of testicular cells, probably being involved in
CC spermatogenesis. It can be used to detect ligands promoting proliferation
CC and/or differentiation of such cells in cultures and may also be used to
CC treat infertility. Antagonists of this receptor may be used to
CC characterise ligand-receptor interactions and as male-specific
CC contraceptives. By blocking the action of IL-13, receptor antagonists and
CC ligand-binding this receptor can also be used to modulate immune
CC function, e.g. in allergy and asthma, as a diagnostic to determine
CC circulating levels of ligand and also to isolate and purify ligands.
CC Antibodies can be used to assay circulating receptor (an abnormal level
CC may be indicative of disease such as cancer), for labelling cells that
CC express the receptor, and therapeutically as antagonist.
XX Sequence 372 AA;
XX

Query Match 91.7%; Score 1718; DB 18; Length 372;
Best Local Similarity 93.5%; Pred. No. 1.1e-160;
Matches 314; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
Qy 1 MAFVCLAIAGCLYFLISTFGCTSSDTEIKVNPQDFEIVDPGILGYLQWQPLSLD 60
Db 1 mafvclaiagcltflistfgtststetkikvnpqdfvdpvgylylqwpplslid 60
Qy 61 HFKECTVEVELKYNIGSETWKTITTKNLHYKDGFDLNGIEAKIHTLLPWQCTNGSEVO 120
Db 61 nfkectveyelkynigsetwtitknlhykdgfdlنگieakhtllpwqctngsevg 120
Qy 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNVLNFWYBGLD 180
Db 121 sswaetywispgipetkvqdmcdvynnyqyllcswkpgigvlltdnynlwyegldr 180
Qy 181 ALQCVDYIKADGONIGCRFPYLEADYKDFYICVNGSSENKPIRSSVFTFOLNIVKPLP 240
Db 181 alqcvdyikdgognigrcrfpylesdykdfyicvngssetkpirssvftfqlnkvkplp 240
Qy 241 PVLVLTFTRESSCEIKLWSIPGLPIPARCFDYIEIREDDTLTIVATVENETTLKTTNE 300
Db 241 pvlclctdeslyelkikwsipglpircfveyelredtltlvtvtenetytlkittne 300
Qy 301 TROLCFVRSKVNICYSDGCIWSEWSDKQCWEGEDL 336
Db 301 trqlcfvrskvnicycsddgciwsewsdkqcwveel 336
RESULT 14
AAW35294

AAW35294 standard; Protein; 383 AA.
AAW35294;
27-MAR-1998 (first entry)
Murine IL-13 binding chain of the IL-13 receptor.
Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
allergy; asthma; immune complex disorder.
Mus sp.
Key Location/Qualifiers
Peptide 1..21
Protein /label= signal_sequence
22..383 /note= "putative"
Domain /label= mature_protein
22..334
Domain /label= extracellular_domain
335..356
Domain /label= transmembrane_domain
357..383
Domain /label= intracellular_domain
W09731946-A1.
04-SEP-1997.
28-FEB-1997; 97WO-US03124.
01-MAR-1996; 96US-0609572.
(GEMY) GENETICS INST INC.
Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
Wood C;
WPI; 1997-448632/41.
N-PSDB; AAT75213.
New nucleic acid encoding interleukin-13 receptor binding chain and
transformed cells - proteins, antibodies and inhibitors, for
treating immunoglobulin E-mediated diseases, e.g. Graves disease,
and in diagnosis
Claim 11; Pages 30-31; 49pp; English.
The present sequence represents the murine interleukin-13 (IL-13) binding
chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
mediator of the known biological activities of IL-13. Recombinant
IL-13bc proteins, and antibodies raised against them, are used to
inhibit the binding of IL-13 to its receptor. They are particularly used
to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
They are also used to treat immune deficiency (particularly in
haematopoietic progenitor cells), cancer etc., and to increase macrophage
activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
with such activity is combined with IL-13bc and the mixture applied,
in vivo, to a cell expressing at least one chain of the IL-13 receptor
other than IL-13bc. IL-13bc can also be used in diagnosis to detect
expression of IL-13, its receptor or binding chain, and to raise specific
antibodies which may be useful for treating some tumours.
Sequence 383 AA;
Query Match 63.2%; Score 1184; DB 18; Length 383;
Best Local Similarity 64.0%; Pred. No. 3 Re-108;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYTELISTFGCTSSDTEIKVNPQDFEIVDPGLGYLYLQWPPPLSLD 60
DB 1 mafv--hircfcilclctitgys---leikvnpqdfelidpglylylqwkppvvie 54
QY 61 HFKECTVEYELKYRNIGSETWKTITITNHLHYKDGFDLNGIEAKIHLLPWOCTNGSEVQ 120
DB 55 kfgctleyelkyrnvdswktititnlykdgfdlnkglegktrhlshcctngsevg 114
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYWVEGLDH 180
DB 115 spwleasygidegslecktqdmkclvynwqylvcswkpgktvysdntnftfveglh 174
QY 181 ALQCVDIKADGQNGIRFPYLEASDYKDYICVNGSSENKPIRSYFTFOLQNVKPLP 240
DB 175 alqcadylqdeknvgcklnldssdykdficvngsklepirssyftvqlqnvkplp 234
QY 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYETREDDTTLVTATVENTYTLKTTNE 300
DB 235 peflhisvensidirmkwstpggpiprcyeyeiaveddiswesatdkndmkikrrane 294
QY 301 TROLCFVVRKVNLYCSDGGINSEMSDKQWEG 333
DB 295 sedicffvrckvnlcyaddgiwsewseeecweg 327
RESULT 15
AAV95295
ID AAV95295 standard; Protein; 383 AA.
AC AAV95295;
XX
DT 12-SEP-2000 (first entry)
DE IL-13 binding chain of mouse IL-13 receptor.
XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; anti-allergic;
KW antiinflammatory; antiasthmatic; vaccine.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
22..383
FT Domain /note= "mature protein"
22..334
FT Domain /note= "extracellular domain; a polypeptide
comprising amino acids 22-334 is
specifically claimed in Claim 11(b)"
FT Domain 335..356
FT Domain /note= "transmembrane domain"
357..383
FT Domain /note= "intracellular domain; a polypeptide
comprising amino acids 257-383 is
specifically claimed in Claim 11(c)"
XX
PN W0200036103-A1.
XX
PD 22-JUN-2000.
XX
PF 13-DEC-1999; 99WO-US29493.
XX
PR 14-DEC-1998; 98US-0211335.
XX
PA (GEMY) GENETICS INST INC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;
XX

[illegible]

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:08:36 ; Search time 35.33 Seconds
(without alignments)
196.404 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873
Sequence: 1 MAFVCLAIGCLYTLISTTF.....DDGIWSEWSKQCEGDEL 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 1873 | 100.0 | 380 | 1 US-08-609-572-4 | Sequence 4, Appli |
| 2 | 1873 | 100.0 | 380 | 4 US-08-841-751-4 | Sequence 4, Appli |
| 3 | 1873 | 100.0 | 380 | 4 US-08-846-340-4 | Sequence 4, Appli |
| 4 | 1184 | 63.2 | 383 | 1 US-08-609-572-2 | Sequence 2, Appli |
| 5 | 1184 | 63.2 | 383 | 4 US-08-841-751-2 | Sequence 2, Appli |
| 6 | 1184 | 63.2 | 383 | 4 US-08-846-340-2 | Sequence 2, Appli |
| 7 | 293.5 | 15.7 | 420 | 1 US-07-757-390-13 | Sequence 13, Appl |
| 8 | 293.5 | 15.7 | 420 | 1 US-08-442-282-13 | Sequence 13, Appl |
| 9 | 293.5 | 15.7 | 420 | 1 US-08-442-281-13 | Sequence 13, Appl |
| 10 | 293.5 | 15.7 | 420 | 1 US-08-939-727-13 | Sequence 13, Appl |
| 11 | 293 | 15.6 | 313 | 3 US-08-836-561-106 | Sequence 106, App |
| 12 | 292.5 | 15.6 | 396 | 1 US-07-757-390-14 | Sequence 14, Appl |
| 13 | 292.5 | 15.6 | 396 | 1 US-08-442-282-14 | Sequence 14, Appl |
| 14 | 292.5 | 15.6 | 396 | 1 US-08-442-281-14 | Sequence 14, Appl |
| 15 | 292.5 | 15.6 | 396 | 2 US-08-939-727-14 | Sequence 14, Appl |
| 16 | 292 | 15.6 | 335 | 1 US-07-947-130-2 | Sequence 2, Appli |
| 17 | 292 | 15.6 | 335 | 1 US-08-421-822-2 | Sequence 2, Appli |
| 18 | 292 | 15.6 | 335 | 1 US-08-421-823-2 | Sequence 2, Appli |
| 19 | 285 | 15.2 | 427 | 4 US-08-969-125-9 | Sequence 9, Appli |
| 20 | 229 | 12.2 | 315 | 1 US-07-757-390-8 | Sequence 8, Appli |
| 21 | 229 | 12.2 | 315 | 1 US-08-442-282-8 | Sequence 8, Appli |
| 22 | 229 | 12.2 | 315 | 1 US-08-442-281-8 | Sequence 8, Appli |
| 23 | 229 | 12.2 | 315 | 2 US-08-939-727-8 | Sequence 8, Appli |
| 24 | 229 | 12.2 | 332 | 1 US-07-757-390-7 | Sequence 7, Appli |
| 25 | 229 | 12.2 | 332 | 1 US-08-442-282-7 | Sequence 7, Appli |
| 26 | 229 | 12.2 | 332 | 1 US-08-442-281-7 | Sequence 7, Appli |
| 27 | 229 | 12.2 | 332 | 2 US-08-939-727-7 | Sequence 7, Appli |

Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 11, Appli
Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-609-572-4

Query Match 100.0%; Score 1873; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.1e-186;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTLISTTFCTSSSTTEIKVNPQDFEIVDPGVLGYLQWQPLSLD 60

|||||
Db 1 MAFVCLAIGCLYTLFTTGCSSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
QY 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFOLQNIKPLP 240
Db 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFOLQNIKPLP 240
QY 241 PVLFTFTRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTITNE 300
Db 241 PVLFTFTRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTITNE 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337

RESULT 2

US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-751-4

Query Match

100.0%; Score 1873; DB 4; Length 380;

Best Local Similarity 100.0%; Pred. No. 3.1e-186;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTLFTTGCSSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLFTTGCSSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
QY 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFOLQNIKPLP 240
Db 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFOLQNIKPLP 240
QY 241 PVLFTFTRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTITNE 300
Db 241 PVLFTFTRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTITNE 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337
RESULT 3
US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-846-340-4

Query Match 100.0%; Score 1873; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.1e-186;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLFTSTFGCTSSSDPEIKVNPQDPFEIVDPGVLGYLYLQWOPPLSLD 60
Db 1 MAFVCLAIGCLYTLFTSTFGCTSSSDPEIKVNPQDPFEIVDPGVLGYLYLQWOPPLSLD 60

Qy 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNKKGIEAKIHTLLPQCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNKKGIEAKIHTLLPQCTNGSEVQ 120

Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWOYLCSWKPGIGVLLDTNINFLFYWYEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVDMDCVYNNWOYLCSWKPGIGVLLDTNINFLFYWYEGLDH 180

Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Db 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240

Qy 241 PVLTFTRSSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
Db 241 PVLTFTRSSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300

Qy 301 TROLCFVVRKVNIIYCSDDGIWSEWSKQCEGDL 337
Db 301 TROLCFVVRKVNIIYCSDDGIWSEWSKQCEGDL 337

RESULT 4

US-08-609-572-2
; Sequence 2, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-609-572-2

Query Match 63.28; Score 1184; DB 1; Length 383;
Best Local Similarity 64.0%; Pred. No. 1.1e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

Qy 1 MAFVCLAIGCLYTLFTSTFGCTSSSDPEIKVNPQDPFEIVDPGVLGYLYLQWOPPLSLD 60
Db 1 MAFV--HRCCLCFLLCTITGYS-----LEIKVNPQDPFEIILDPGLLGYLYLQWPPVWIE 54

Qy 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNKKGIEAKIHTLLPQCTNGSEVQ 120
Db 55 KFKGCTLEYELKYRNIVSDSKWTITITRNLIYKDGFDLNKKGIEGKIRTHLSEHCTNGSEVQ 114

Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWOYLCSWKPGIGVLLDTNINFLFYWYEGLDH 180
Db 115 SPWIEASYGISDEGSLETKIQDMKCIYYNNWOYLCSWKPGKTVSDTNMTFFWYEGLDH 174

Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Db 175 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 234

Qy 241 PVLTFTRSSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
Db 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLKRANE 294

Qy 301 TROLCFVVRKVNIIYCSDDGIWSEWSKQCEG 333
Db 295 SEDLCFFVRKVNIIYCADDDGIWSEWSEECWEG 327

RESULT 5

US-08-841-751-2
; Sequence 2, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-841-751-2

Query Match 63.2%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 1.1e-114; Indels 6; Gaps 2;
Matches 213; Conservative 46; Mismatches 68

QY 1 MAFVCLAIGCLYTLSTTFCCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPVLSLD 60
Db 1 MAFV--HIRCLCFLLCITGYS----LEIKVNPQDFEILDPLGLGYLYLQWQPPVIVIE 54
QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHTLLPQCTNGSEVQ 120
Db 55 KFEGCTLEYELKYRNVDSDSKTITITRNLHYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGLGVLLDTNLYNLFYWEGLDH 180
Db 115 SPWIEASGIGDESLETKIDMKCIYNNWQYLLCSWKPGLGVLLDTNLYNLFYWEGLDH 174
QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSKLEPIRSSYTFVQLQNVKPLP 240
Db 175 ALQCADYLQHDKEKNVGVKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTFVQLQNVKPLP 234
QY 241 PVYLTFRESCEIKLWSIPGLPIPARCFDYEIEIRDDTTLTAVTAVENETYLKTTNE 300
Db -235 PEFHLISVENSIDIRMKWSTPGGPIPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEWEG 333
Db 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEG 327

RESULT 6
US-08-846-340-2
Sequence 2, Application US/08846340
Patent No. 6248714

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A. 32,724
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: G15268

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-2

Query Match 63.2%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 1.1e-114; Indels 6; Gaps 2;
Matches 213; Conservative 46; Mismatches 68

QY 1 MAFVCLAIGCLYTLSTTFCCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPVLSLD 60
Db 1 MAFV--HIRCLCFLLCITGYS----LEIKVNPQDFEILDPLGLGYLYLQWQPPVIVIE 54
QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHTLLPQCTNGSEVQ 120
Db 55 KFEGCTLEYELKYRNVDSDSKTITITRNLHYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGLGVLLDTNLYNLFYWEGLDH 180
Db 115 SPWIEASGIGDESLETKIDMKCIYNNWQYLLCSWKPGLGVLLDTNLYNLFYWEGLDH 174
QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSKLEPIRSSYTFVQLQNVKPLP 240
Db 175 ALQCADYLQHDKEKNVGVKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTFVQLQNVKPLP 234
QY 241 PVYLTFRESCEIKLWSIPGLPIPARCFDYEIEIRDDTTLTAVTAVENETYLKTTNE 300
Db 235 PEFHLISVENSIDIRMKWSTPGGPIPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEWEG 333
Db 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEG 327

RESULT 7
US-07-757-390-13
Sequence 13, Application US/07757390
Patent No. 5453491
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomimaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:


```
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-757-390-13

Query Match      15.7%; Score 293.5; DB 1; Length 420;
Best Local Similarity 28.1%; Pred. No. 3.4e-22;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;
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| QY | 27 | DTEIKVNPDPDEIVDPSGYLGYLWQPPLSLDHDFKECTVEVELKYRNITGSETWKTIIT | 86 : : : : : : : : : : : : : : : : |
| DB | 25 | DELKISLPVPNTTKVTG-LAQLVLWKPNPDQEQ-RNVNLXYQVKINAPKEDDDYEIRIT | 82 : : : : : : : : : : : : : : : : |
| QY | 87 | KNLHYKDGFGLINKIGIEAKIHTLLPWCQTNGSEVOSSNAETTYTWSPOCIPETKVQDMDCV | 146 : : : : : : : : : : : : : : : : : |
| DB | 83 | ES---KCVTILHKGFSAVSRTILO---NDHSLCLASSASAELH-APGSPGTSVVNLTCT | 135 : : : : : : : : : : : : : : : : : |
| QY | 147 | -----YYNQYLL-CSWRPGIGVLDTNNLRY----WYEGLDHALQCVDVIKAD | 191 : : : : : : : : : : : : : : : : |
| DB | 136 | TNTTEDNYSRLRSYQSLSLCHCTLWLVGTPAPEQTFLFYRYGSWTE-----ECQEYSKDT | 189 : : : : : : : : : : : : : : : : : |
| QY | 192 | -GVNICGRFP--YLEASDYKDFICVNGSSENKENPIRSSYTFQLQNIVKPPLPPVLTETR | 248 : : : : : : : : : : : : : : : : |
| DB | 190 | LGRNIACWFPRFTFLSKGRDWLAIVLVNGSSKHSAIRPFQDLFALHAIDQINPPLNVTAEI | 249 : : : : : : : : : : : : : : : : : |
| QY | 249 | ESSCEIKLKSIPLGPARGFDYEIREDDTLTVATVENETYTLKTNETRQLCFVV | 308 : : : : : : : : : : : : : : : : |
| DB | 250 | EGT-RLSQHEKPVSPAIPHCFDYEVAIHNRNGYLQIEKLMTAFISIDDL SKYDVQV | 308 : : : : : : : : : : : : : : : : |
| QY | 309 | RSKVNIYCSDDGIIWEUSD KOCWGED 335 | |
| DB | 309 | RAAVSSMCREAGLWSEWS-QPIYVGN D 334 | |

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RESULT 8
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-13

Query Match 15.7%; Score 293.5; DB 1; Length 420;
Best Local Similarity 28.1%; Pred. No. 3.4e-22;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

QY 27 DTEIKVNPDPDFEIVDPGLYLYLQWOPPLSLDHFKECTVEYELKYNIGSETWKTIT 86
Db 25 DEKISLLPPVNFITKVVG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
QY 87 KNLHYKQGFDLNKGIEAKIHTLLPWQCTNGSEVSSWAETTYTWSPOGIPETKYQDMDCV 146
Db 83 ES---KCVTILHKGFSAVRITLQ---NDHSLASSWASAEHL-APPGSPGTSVNNLTCT 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF----WYEGDLHALQCVDIKAD 191
Db 136 TTTTDDNYSLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -QONIGCRFP--YLEASDYKDFYICVNGSSNKPPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRNIACWFPTFTLSKGRDLAVLVNGSSKHSAIRPFDQLFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPPIPARCFDYEIREDDTTLVATVENETTYTLKTNETQLCFV 308
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEKIHNRNGYLQTEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESKOCWEGED 335
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGN 334

RESULT 10
US-08-939-727-13
; Sequence 13, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-939-727-13

Query Match 15.7%; Score 293.5; DB 2; Length 420;
Best Local Similarity 28.1%; Pred. No. 3.4e-22;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

QY 27 DTEIKVNPDPDFEIVDPGLYLYLQWOPPLSLDHFKECTVEYELKYNIGSETWKTIT 86
Db 25 DEKISLLPPVNFITKVVG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
QY 87 KNLHYKQGFDLNKGIEAKIHTLLPWQCTNGSEVSSWAETTYTWSPOGIPETKYQDMDCV 146
Db 83 ES---KCVTILHKGFSAVRITLQ---NDHSLASSWASAEHL-APPGSPGTSVNNLTCT 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF----WYEGDLHALQCVDIKAD 191
Db 136 TTTTDDNYSLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -QONIGCRFP--YLEASDYKDFYICVNGSSNKPPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRNIACWFPTFTLSKGRDLAVLVNGSSKHSAIRPFDQLFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPPIPARCFDYEIREDDTTLVATVENETTYTLKTNETQLCFV 308
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEKIHNRNGYLQTEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESKOCWEGED 335
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGN 334

RESULT 11
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiko
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
```


; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-14

Query Match 15.6%; Score 292.5; DB 2; Length 396;
Best Local Similarity 27.8%; Pred. No. 4e-22;
Matches 91; Conservative 58; Mismatches 143; Indels 35; Gaps 13;

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|----|-----|---|
| Qy | 27 | DTEIKVNPDPQFEIVDPGYLVYLQWQPLSLDHFKECTVEYELKYRNIQSGETWKTIT 86 |
| Db | 25 | DEKISLLFPVNETIKVTG-LAQVLLQWKPNDQEQ-RVNVLEYQVKINAPKEDDYETRIT 82 |
| Qy | 87 | KNLHYKDGFDLNGKEAKIHTLLPQCCTNGSEVQSSMAETTYWISPGQIPETKYQDMDCV 146 |
| Db | 83 | ES---KCVTILHKGFSAVRLIQ---NDHSLASSWASAEHL-APPGSPGTSIVNLFTCT 135 |
| Qy | 147 | -----YYNQYLL-CSWKPGIGVLLDTNLYF----WYEGLDHALQCVDIYKAD 191 |
| Db | 136 | TNTTENDYNSRLRSQVSLHCTWLVTGDPEDTQYFLYYRYGSWTE-----ECOEYSKDT 189 |
| Qy | 192 | -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKVPPLPPVLTETR 248 |
| Db | 190 | LGRNIACWFPPTFILSKGRDMLNLVNGSSKHSARPPDQFLALHAIQINPPLNVTAEI 249 |
| Qy | 249 | ESSCEIKLKWISPLGPIPARCFYEIEIREDDTTLTATVENETYYTKTNTETROLCEFW 308 |
| Db | 250 | EGT-RLSIQWEKPKVSAPFIHCFDVEVKIHNTRNGYLOIEKLTNAFISIIDLSKYDVQV 308 |
| Qy | 309 | RSKVNICYSDDGWSEWSKOCWEGED 335 |
| Db | 309 | RAAVSSMCREAGLWSEWS-QPIYVGN 334 |

Search completed: September 1, 2001, 19:08:37
Job time: 164 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:58 ; Search time 24.79 seconds
(without alignments)
525.094 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: 2104

Sequence: 1 MAFVCLAIGCLYFLISTTF.....LLLRKPNTPKMIPEFFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Score | Match Length | ID | Description |
|------------|-------------|--------------|--------------|---------------------|
| 1 | 2104 | 100.0 | 1 IL32_HUMAN | Q14627 homo sapien |
| 2 | 310.5 | 14.8 | 1 IL5R_HUMAN | Q01344 homo sapien |
| 3 | 298 | 14.2 | 1 IL31_MOUSE | O09030 mus musculus |
| 4 | 295.5 | 14.0 | 1 IL31_HUMAN | P78552 homo sapien |
| 5 | 263 | 12.5 | 1 PRLR_CHICK | Q04594 gallus gall |
| 6 | 247 | 11.7 | 1 IL5R_MOUSE | P21183 mus musculus |
| 7 | 238 | 11.3 | 1 PRLR_MELGA | Q91094 meleagris g |
| 8 | 220 | 10.5 | 1 CYRG_HUMAN | P31785 homo sapien |
| 9 | 216.5 | 10.3 | 1 PRLR_COLLI | Q90374 columba liv |
| 10 | 212.5 | 10.1 | 1 CYRG_MOUSE | P34902 mus musculus |
| 11 | 208 | 9.9 | 1 CYRG_CANFA | P40321 canis famil |
| 12 | 195 | 9.3 | 1 IL3B_MOUSE | P26954 mus musculus |
| 13 | 189.5 | 9.0 | 1 CYRG_BOVIN | Q95118 bos taurus |
| 14 | 178.5 | 8.5 | 1 CYRG_MOUSE | P32927 mus sapien |
| 15 | 173.5 | 8.2 | 1 CYRG_MOUSE | P26955 mus musculus |
| 16 | 165 | 7.8 | 1 PRLR_BOVIN | Q28172 bos taurus |
| 17 | 165 | 7.8 | 1 PRLR_RAT | P05710 rattus norv |
| 18 | 159 | 7.6 | 1 PRLR_MOUSE | Q08501 mus musculus |
| 19 | 151 | 7.2 | 1 PRLR_HUMAN | P16471 homo sapien |
| 20 | 151 | 7.2 | 1 IL2S_HUMAN | Q99665 homo sapien |
| 21 | 150.5 | 7.2 | 1 IL6B_MOUSE | Q00560 mus musculus |
| 22 | 150 | 7.1 | 1 PRLR_CEREL | Q28235 cervus elap |
| 23 | 149 | 7.1 | 1 PRLR_RABIT | P14787 oryctolagus |
| 24 | 142.5 | 6.8 | 1 GMCR_HUMAN | P15509 homo sapien |
| 25 | 138 | 6.6 | 1 IL3R_HUMAN | P26951 homo sapien |
| 26 | 134.5 | 6.4 | 1 LIFR_HUMAN | P42702 homo sapien |
| 27 | 131.5 | 6.2 | 1 PRLR_ORENI | Q91513 oreochromis |
| 28 | 128 | 6.1 | 1 IL2S_MOUSE | P97378 mus musculus |
| 29 | 126.5 | 6.0 | 1 IL6B_HUMAN | P40189 homo sapien |
| 30 | 120.5 | 5.7 | 1 GCSR_HUMAN | Q99062 homo sapien |
| 31 | 113.5 | 5.4 | 1 LEPR_HUMAN | P48357 homo sapien |
| 32 | 112.5 | 5.3 | 1 PTP1_DROME | P35992 drosophila |
| 33 | 109.5 | 5.2 | 1 IL6B_RAT | P40190 rattus norv |

ALIGNMENTS

| RESULT | ID | IL32_HUMAN | STANDARD; | PRT; | 380 AA. |
|--------|--|-----------------------------------|-------------|------|---------|
| AC | Q14627 | O00667; | | | |
| DT | 01-NOV-1997 | (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 | (Rel. 35, Last sequence update) | | | |
| DT | 30-MAY-2000 | (Rel. 39, Last annotation update) | | | |
| DE | INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 DE BINDING PROTEIN). | | | | |
| GN | IL13RA2 OR IL13R. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Renal cell carcinoma; | | | | |
| RX | MEDLINE=96279273; PubMed=8663118; | | | | |
| RA | Caput D., Laurent P., Kagnad M., Lelias J.M., Lefort S., Vita N., Ferrara P.; | | | | |
| RT | "Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain."; | | | | |
| RL | J. Biol. Chem. 271:16921-16926(1996). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Testis; | | | | |
| RA | Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.; | | | | |
| RL | Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases. | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Brain; | | | | |
| RX | MEDLINE=97321053; PubMed=9177784; | | | | |
| RA | Guo J., Apiou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.; | | | | |
| RT | "Chromosome mapping and expression of the human interleukin-13 receptor."; | | | | |
| RL | Genomics 42:141-145(1997). | | | | |
| CC | -1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13). BUT NOT TO IL-4. | | | | |
| CC | -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. | | | | |
| CC | -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN. | | | | |
| CC | -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. | | | | |
| CC | ----- | | | | |
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| CC | ----- | | | | |
| DR | EMBL; | X95302; | CAA64617.1; | -; | |
| DR | EMBL; | U70981; | AAB17170.1; | -; | |
| DR | EMBL; | Y08768; | CAA70021.1; | -; | |
| DR | MTM; | 300130; | -; | -; | |

P10912 homo sapien
P40223 mus musculus
P79108 bos taurus
Q28575 ovis aries
P04884 vesicular s
P42703 mus musculus
P19756 sus scrofa
P19941 oryctolagus
O62959 rattus norv
P14753 mus musculus
P16310 rattus norv
P48356 mus musculus

34 107.5 5.1 638 1 GHR_HUMAN
35 107.5 5.1 837 1 GCSR_MOUSE
36 107 5.1 634 1 GHR_BOVIN
37 106 5.0 634 1 GHR_SHEEP
38 105 5.0 511 1 VGLG_VSVO
39 104.5 5.0 1092 1 LIFR_MOUSE
40 102.5 4.9 638 1 GHR_PIG
41 101.5 4.8 638 1 GHR_RABIT
42 99.5 4.7 1162 1 LEPR_RAT
43 99 4.7 507 1 EPOR_MOUSE
44 99 4.7 638 1 GHR_RAT
45 98.5 4.7 1162 1 LEPR_MOUSE

```

DR InterPro: IPR001777; -
DR InterPro: IPR002465; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;

Query Match 100.0%; Score 2104; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTFCTSSDTEIKVNPQDPFIVDPGVLGYLQWQPPLSLD 60
DB 1 MAFVCLAIGCLYTLSTFCTSSDTEIKVNPQDPFIVDPGVLGYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
DB 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
QY 121 SSWAETTYWISQGIPTKVDMDCVYNNQYLLCSKWPKGVLGVDNLYNLFYWEGLDH 180
DB 121 SSWAETTYWISQGIPTKVDMDCVYNNQYLLCSKWPKGVLGVDNLYNLFYWEGLDH 180
QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQQLQNVKPLP 240
DB 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQQLQNVKPLP 240
QY 241 PVYLTFRESSECEIKLWISPLGIPARCFDYEIEIRDDTTLTAVENTYTLKTTNE 300
DB 241 PVYLTFRESSECEIKLWISPLGIPARCFDYEIEIRDDTTLTAVENTYTLKTTNE 300
QY 301 TRQLCFVVRSVNVIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFGLILVIFVTG 360
DB 301 TRQLCFVVRSVNVIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFGLILVIFVTG 360
QY 361 LLLRKPNTYPKMPEFFCDT 380
DB 361 LLLRKPNTYPKMPEFFCDT 380

RESULT 2
IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125
DE ANTIGEN).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
[2]

```

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RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of
RL the human interleukin 5 receptor alpha subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
[3]
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=9205669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT an IL5-specific alpha chain and a beta chain shared with the receptor
RL for GM-CSF.";
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide cdw125 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M96652; AAA59152.1; -
DR EMBL: M96651; AAA59151.1; -
DR EMBL: M75914; AAA36110.1; -
DR EMBL: A26249; CAA01793.1; -
DR EMBL: A24587; CAA01731.1; -
DR EMBL: A26251; CAA01794.1; -
DR PIR: A40267; A40267.
DR MIM: 147851;
DR InterPro: IPR000950; -
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 343 362 POTENTIAL.
FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).
FT VARSPPLIC 336 420 MISSING (IN SOLUBLE ISOFORM S1).
FT VARSPPLIC 333 333 N -> K (IN SOLUBLE ISOFORM S2).
FT VARSPPLIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
SQ SEQUENCE 420 AA; 47700 MW; 420881FEC6B51700 CRC64;

Query Match 14.8%; Score 310.5; DB 1; Length 420;
Best Local Similarity 26.6%; Pred. No. 3.9e-18;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDPFIVDPGVLGYLQWQPPLSLDHFKECTVEYELKYNIGSETWKTIT 86
DB 25 DEKISLLPPVNFITKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82

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IL4R alpha of a functional IL-4/IL-13 receptor complex.";
 [2] FEBS Lett. 401:163-166(1997).
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
 RA Jeunin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
 RA Euster H.P., Bonnefoy J.Y.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-T-cell;
 RX MEDLINE=97067184; PubMed=9910586;
 RA Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
 RA Leonard W.J.;
 RT "cDNA cloning and characterization of the human interleukin 13
 RT receptor alpha chain.";
 RL J. Biol. Chem. 271:29265-29270(1996).
 [4]
 RN
 RP SEQUENCE FROM N.A.
 RA Wada M., Hisano T., Kuwano M.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
 CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
 CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
 CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
 CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
 CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
 CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
 CC SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
 CC KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC
 DR EMBL; Y10659; CAA71669.1; -
 DR EMBL; Y09328; CAA70508.1; -
 DR EMBL; U62858; AAB37127.1; -
 DR EMBL; U81379; AAD00510.3; -
 DR HSSP; P31785; IILN.
 DR MIN; 300119; -
 DR InterPro; IPR001777; -
 DR Pfam; PF00041; fn3; 1.
 DR PROSITE; PS01356; HEMATOPOI_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 427
 FT DOMAIN 22 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 427
 FT DOMAIN 39 102
 FT DISULFID 46 95
 FT DISULFID 134 144
 FT DISULFID 173 185
 FT CARBOHYD 37 37
 FT CARBOHYD 61 61
 FT CARBOHYD 105 105
 FT CARBOHYD 138 138
 FT CARBOHYD 157 157
 FT CARBOHYD 235 235
 FT CARBOHYD 265 265
 FT CARBOHYD 293 293
 FT CARBOHYD 329 329

FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 130 130 T -> I (IN REF. 3).
 FT CONFLICT 358 358 G -> D (IN REF. 3).
 SQ SEQUENCE 427 AA; 48759 MW; 5983B3E8F554107B CRC64;
 Query Match 14.0%; Score 295.5; DB 1; Length 427;
 Best Local Similarity 26.0%; Pred. No. 6.7e-17;
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;
 QY 11 LYTELISTFTGCTSSSTTEIKVNPDPQFEIVDPGYLYLYLOWOPPLSLDHFKECTVEY- 69
 DB 10 LWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTPNPPEGAS--SNCSLWYF 67
 QY 70 ---ELRYNIGSETWKTIIITKLNHYKDGFDLNKIEAKIHTLLPWQC-TNGSEVOSSWA 124
 DB 68 SHFGDKQDKKIAPETRRSI-----EVLNERICIQVGS---QCSTNESEKPSILV 114
 QY 125 ETTYWIS-PQGITETKVQDMDCVYVNMQYLCSMKPGIGVLLDTNLYNFYWEGLDHALQ 183
 DB 115 EKC--ISPPEGDPESATVETLOCIIWHNLSYMKCSWLPGRNTSPDINLYLYWHSLEKIHQ 172
 QY 184 CVDYKADQGNIGRFPYLEASD--YKDFYICVNGSSSENKPIRSYFTFQIQNTVKKPLPP 241
 DB 173 C-ENIFREGQVFGCSFDLTQVKDSSFQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP 231
 QY 242 --VLTFTRESSCEIKLWSITPLGPIPARCFDYEIEIREDDTT-----LVTAIVENETY 293
 DB 232 HIKNLSFHND---DLYVQWENPQNF-I-SRCLFYEVVNNQSQTETHNVFYVQAEKCNPEF 287
 QY 294 TLKNTNTRQLCFVY-----RSKNVIYC--SDGIWSEWSDKQCEGEDLSKK 339
 DB 288 ERNVENTS---CFMVGVPDPTLNTVIRVTKNLCLYEDDKLWSNQEM-----S1GKK 339
 QY 340 TLLRFWLPP-----GFTLLIVFVTGL--LLRKNPTYP-KMIEFFEDF 379
 DB 340 RNSTLYITMLLIVPVIVAGIIVLLLYLKLKLIIFPPIDPDPGKIFKEMFGD 391
 RESULT 5
 ID PRLR_CHICK STANDARD; PRT; 831 AA.
 AC Q04594;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
 GN PRLR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;
 RX MEDLINE=93075121; PubMed=1445292;
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
 RT "Double antenna structure of chicken prolactin receptor deduced from
 RT the cDNA sequence.";
 RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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CC EMBL; D13154; BAA02439.1;
DR PIR; JQ1655;
DR HSSP; JQ1671; 18p3.
DR InterPro; IPR000950;
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT CARBOHYD 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
FT SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADBE9 CRC64;

Query Match 12.5%; Score 263; DB 1; Length 831;
Best Local Similarity 26.4%; Pred. No. 6.7e-14;
Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

OY 18 TFGCTSSDTEIKVN--PPDQFE---IVDPG-----YLVGLYLQWOPPLSL 59
DB 97 TFFNTVATNEIGNSDDPQVDVTSIVQGPSVNLFLTKRSANIMYLAKWSPPLLA 156

OY 60 DHFKECTVEYELKYNIGSETWTKITIKNLHYKDFGLDKGIEAKIHTLLPQCTNGSEV 119
DB 157 DASSNHLHYELRIKPEEKWEETI---SVGVQTOCKINR-LNAGMRVYVQVRCCTDPGE 212

OY 120 QSSWAETTYWISPOG-IPETKVQDMDCVYNNQWYLLCSWKPGIGVLLDTNINLFWYEG 178
DB 213 WSESSERHILIPGSGPPEKPTTIKCRSPEKETFTCWKPKGLDGGHPNTYLLYSKEGE 272

OY 179 DHALQCVDIKADGONIGCRFPYLEADYKDFYICVNGSSSENKPIRSSYFTFQIQNVKP 238
DB 273 EQVIECPDY-RTAGFN-SCYFDKHKITSFTWYINIVTRATNEMGNSSDPHYVDVYIVQP 330

OY 239 LPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR---EDDTLTIVATYEN 290
DB 331 DPPVAVTLELKKPINRKPVLVLTWSPPLADVRSGWLTLEYELRLKPEGEWETIFVGQ 390

OY 291 ET-YLTKTNTETRLQCFVVRKSNVNYCSD--GIWSESDKQCWE-GEDLSKKLLLRWL 346
DB 391 QTYKMFSLNPGKKYI-----IQHCKPDHHSWSESSENYIQIPNDFRVKMI-VVI 443

OY 347 PFGFTI--LILVFTGLLRKPNTPYKMP 374
DB 444 VLGVLSLILIMSWTVLKGKRMITFMLP 473

RESULT 6
ID IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)

or send an email to license@isb-sib.ch).
-----
DT DE 15-JUL-1999 (Rel. 38, Last annotation update)
GN IL5RA OR IL5R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA Takatsu K.;
RT "Molecular cloning and expression of the murine interleukin-5
RT receptor.";
RL EMOB J. 9:4367-4374(1990).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC ON B-CELLS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90205; BAA14231.1;
DR PIR; S12357; S12357.
DR MGD; MGI:96558; Il5ra.
DR InterPro; IPR000950;
DR InterPro; IPR002465;
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415
FT DOMAIN 18 339
FT TRANSMEM 340 361
FT DOMAIN 362 415
FT DISULFID 131 152
FT DISULFID 179 193
FT CARBOHYD 32 32
FT CARBOHYD 128 128
FT CARBOHYD 213 213
FT CARBOHYD 241 241
FT SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 11.7%; Score 247; DB 1; Length 415;
Best Local Similarity 24.6%; Pred. No. 5.9e-13;
Matches 91; Conservative 70; Mismatches 151; Indels 58; Gaps 18;

OY 34 PPQDFEIVDPGYLVLYLQWOPPLSLDHFKECTVEYELKYNIGSETWTKITIKNLHYK 93
DB 29 PPNFTIKATG-LAQVLLHWDPNPDQEQ-RHVDLEYHVKNAPQDEYDTRKTES---KC 83

OY 94 GFDNLKGTEAKIHTLLPQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVYNN--- 149
DB 84 VTPLEHGFPAASVRLTK---SSHTTLASSWSAEI-KAPPGSPGTSVNLCTTHTVVSS 139

OY 150 -----WQY-LICSWKPGIGVLLDTNINLFWYEGDLHALQCVDIK-ADGONIGCRFP- 200
DB 140 HTHLRPYQVSLRCTLWLVGKDAPEDTQYELYRFGVLTE--KQEYSRDALNENTACWFR 197

OY 201 -YLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLPVPVYLTFTRESSCEIKLWS 259
DB 198 TFINSKGFEQLAVHINGSKRAAIKPFQDLSPLAIDQVNPVPRNVTETES-SLYIQWE 256
```

QY 260 IPLGPIPARCFDEYEIRED-----TTLVTATVENETVTLTKTNETROLCPFW 308
 DB 257 KPLSAPDFCHFNELKIYNTXNGHIQKELKANKFISKIDDVSYSIQ-----V 305
 QY 309 RSKVNIYSDGISEWSDKOCWEGEDLSKTKLRFW-----LPGFILLILVIFVYGLLLR 364
 DB 306 RAAVSSPCMPGRNGEWS-QPIYVGKE--RKSLE-VHLVLPAAACFVLLIF--SLICR 359
 QY 365 KNTYPMKIP 374
 DB 360 VCHLWTRLFP 369

RESULT 7
 PRLR_MELGA STANDARD; PRT; 831 AA.
 AC Q91094; Q91091; Q91092;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR).
 GN PRLR.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97057891; PubMed=8902221;
 RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
 RT "Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RT gallopavo.";
 RL Biol. Reprod. 55:1081-1090(1996).
 RN [2]
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RC TISSUE=Ovary;
 RA Pitts G.R., You S.K., Foster D.N., el Halawani M.F.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L76587; AAB01544.1; -;
 DR EMBL; U22947; AAA75038.1; -;
 DR EMBL; U22924; AAA75039.1; -;
 DR HSSP; P16471; IBP3.
 DR InterPro; IPR000950; -;
 DR InterPro; IPR001777; -;
 DR InterPro; IPR002465; -;
 DR Pfam; PF00041; fn3.4;
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438
 FT TRANSMEM 439 459
 FT TRANSMEM 460 831
 FT DOMAIN 25 122
 FT DOMAIN 123 225
 FT DOMAIN 228 325

DOMAIN 326 428
 FT DISULFID 36 46
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 262 262
 FT CARBOHYD 303 303
 FT CARBOHYD 315 315
 FT CARBOHYD 335 335
 SQ SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

Query Match 11.3%; Score 238; DB 1; Length 831;
 Best Local Similarity 26.1%; Pred. No. 7.4e-12;
 Matches 97; Conservative 53; Mismatches 178; Indels 44; Gaps 17;

QY 18 TTFGCTSSDTEIKVN--PPQDFE---IVDPG-----YLGYLWQPPPLSL 59
 DB 97 TTYNITVATNEIGSNSDPOYVDVTSIVQCGSPVNLTEQRYANIMYLWAKSPPLLA 156
 QY 60 DHFRECTVEYELKYRNTGSETWKTIITKNLHYKDGFDLNKIGIEAKIHTLLPWQCTNGSEV 119
 DB 157 DASSNHLHYELRLKPEKEWETV---PVGQVQCKINR-LNAGMRVYVQVRCMLDPGE 212
 QY 120 QSSW-AETTYWISQGIPEIKVQDMDCVYVNWQVLLSKWPGCGIGVLLDTNLTNLYWYEG 178
 DB 213 WSEWSERRILISGLSPPEKPTITKRSPEKETFTCWKFGDGGHPTNTLLYSKE 272
 QY 179 DHALQVDYIKADGONTGCRPPYLEASDYKDFYICVNGSSSENKPIRSSYFFQLQNIKVP 238
 DB 273 EQVTECPDY-RTAGPN-SCYFDKXHTSWTVNITVTRATNEMSGNSDPHYVDVYIVQ 330
 QY 239 LPPVYLFTRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIR-EDDTTLVTATVEN 290
 DB 331 DPPANVTLELKKPINRKPMLTWSPPPLADVRSGWLTLDYELRLKPEEGEWETVFGV 390
 QY 291 ET-YTLKTTNETROLCPVVRKVNIVYCSDD--GIWSEWSKQCWE-GEDLSKKKLLLRWL 346
 DB 391 QTOYKMFSLNPGKYYI-----VQIHCKPDHGSWSESSSENYEIPNDFRVKDMI-VWI 443
 QY 347 PFGFILLIVIEFV 358
 DB 444 VLGVLSSLICLI 455

RESULT 8
 CYRG_HUMAN
 ID CYRG_HUMAN STANDARD; PRT; 369 AA.
 AC P31785;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-
 DE 2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN).
 GN IL2RG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=92335883; PubMed=1631559;
 RA Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,
 RA Munakata H., Nakamura M., Sugamura K.;
 RL "Cloning of the gamma chain of the human IL-2 receptor.";
 RL Science 257:379-382(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93293887; PubMed=8514792;

RA Noguichi M., Adelstein S., Cao X., Leonard W.J.;
 RT "Characterization of the human interleukin-2 receptor gamma chain
 gene.";
 RL J. Biol. Chem. 268:13601-13608(1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
 RX MEDLINE=94004847; PubMed=8401490;
 RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
 RA Willard H., Henthorn P.S.;
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
 RT in X-linked severe combined immunodeficiency, SCID_{HL}.";
 RL Hum. Mol. Genet. 2:1099-1104(1993).
 RN [4]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090315; PubMed=8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 RA Arai K.-I., Sugamura K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 RT receptors for IL-2 and IL-4.";
 RL Science 262:1874-1877(1993).
 RN [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090317; PubMed=8266078;
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguichi M.,
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-4 receptor.";
 RL Science 262:1880-1883(1993).
 RN [6]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE=94090316; PubMed=8266077;
 RA Noguichi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-7 receptor.";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling.";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE=94130970; PubMed=8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding.";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE=94375038; PubMed=8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCID_{HL} that
 RT differentially affect the mRNA processing.";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE=94300093; PubMed=8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency.";
 RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANT XSCID ASN-39.

RX MEDLINE=95023932; PubMed=7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]
 RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE=95397841; PubMed=7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency.";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE=96013903; PubMed=7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Levinsky R.L., Kinnon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis.";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANT XSCID GLN-237 G-H-W INS.
 RX MEDLINE=95164726; PubMed=7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma-chain mutation causing X-linked severe combined
 RT immunodeficiency.";
 RL J. Clin. Invest. 95:895-899(1995).
 RN [15]
 RP VARIANT XSCID GLN-271.
 RX MEDLINE=95190013; PubMed=7883965;
 RA Schmalstieg F.C., Leonard W.J., Noguichi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 RT moderate form of X-linked combined immunodeficiency.";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE=97042245; PubMed=8900089;
 RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells.";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE=97295088; PubMed=9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinnon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation.";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE=98064061; PubMed=9399950;
 RA Sharfe N., Shahar M., Roifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology.";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMAGLOBULINEMIA, SWISS TYPE
 CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

RESULT 11
CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95130114; PubMed=7829104;
RA Henthorn P.S.; Somberg R.L.; Fimiani V.M.; Puck J.M.; Patterson D.F.;
RA Felsburg P.J.;
RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
severe combined immunodeficiency is a homologue of the human
disease.";
RT
RL Genomics 23:69-74(1994).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
SEVERE COMBINED IMMUNODEFICIENCY.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
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CC
CC EMBL; U04361; AAC48403.1; -
DR HSP; P31785; IILN.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 373 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 261 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 262 283 POTENTIAL.
FT DOMAIN 284 373 POTENTIAL.
FT DOMAIN 151 249 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089D8B CRC64;
Query Match 9.9%; Score 208; DB 1; Length 373;
Best Local Similarity 26.0%; Pred. No. 7.9e-10;
Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;
QY 115 NGSE-----VQSSWAETTYWISPGQIPETKVQDMDCVYNNQYLLCSW-----KPGI 161

Db 31 NGNEDITPDEFIATPSET--LSVSLPLPEVQ--CFVFNVEYMNCTWNSSEPR-- 82
QY 162 GVLLDTNINLFYWEGL--DHALQCVDIYIKADGONICRCPPYLEASDYKDFYICVNGSSE 219
Db 83 -----TNLTLYWYKNSNDKQVQECGHLFSREVTTAGCWLQKEEIHLYETFFVVLQDRPRE 137
QY 220 NKPIRSSYFTFQONIVKPLPPVYLTFTRESSCEIKLKWSPILGPIPARCFDYEIREDR 279
Db 138 --PRQSTQKQLQNLVWPAPENLTLHNSELSLSWS---NRHLDHCLHEHVQVVRSD 192
QY 280 -DITLVATVEN-ETYLKTTNTQRCFVVRKSNVNYSCDDGIWSEWSKQCEGWDLS 337
Db 193 WDRSWTEQSVDRHSFSLPSVDGQKFFYFRVRSYRNPCLGSAQRWSEMSPIHW-GSNTS 251
QY 338 KTYLL-----RFWLPFGFILLIVFV 358
Db 252 KENPLFAEAVLPLGSMGLIISLI 276
RESULT 12
IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26934;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN PRECURSOR (COLONY
STIMULATING FACTOR 2 RECEPTOR, BETA 2 CHAIN).
GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90117145; PubMed=2404337;
RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
Yahara I., Arai K., Miyajima A.;
RT "Cloning of an interleukin-3 receptor gene: a member of a distinct
receptor gene family.";
RL Science 247:324-327(1990).
CC -!- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3
RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5
AND GM-CSF RECEPTORS.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M29855; AAA39295.1; -
DR PIR; A40091; A40091.
DR MGD; MGI:1339760; Csf2rb2.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 878 INTERLEUKIN-3 RECEPTOR CLASS II BETA
CHAIN.
FT DOMAIN 23 440 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 441 462 POTENTIAL.
FT DOMAIN 463 878 CYTOPLASMIC (POTENTIAL).

Qy 49 LYLQWQPL---SLDHKECTVEYELKYRNISETWKTIIITKN-----LHYKDGFDLNGK 100
Db 151 FLEWVSLGDAQVSWLSSKDIEFEVAYKRL-QDSWEDAYSILHTSKFOVNEPKLFLPNS 209
Qy 101 IEA-KIHT-LLEPWQCTNGSEVQSSWAETTYWISPOGIPETKVDMDCVYINWOYLLCSWK 158
Db 210 IYAPRVTRLYPGSSLSGR--PSRMSPEAHWDSOPG-DKAQPQNLQCFDFGIGSLHCSWE 266
Qy 159 PGIGVLLDTNLYWYVEGLDHALQCVDIK-ADQONI---GCRFPYLEASDYKDFVIC 213
Db 267 VWTQTGVSFGLYRPSVPAPEEKCSFVKEPPGASVYTRYHCSLPVPEPSAHSQYTVS 326
Qy 214 VNGSENKPIRSSYFTFOLQNIIVPLPPVYLTFTRSSCEIKLWSIPLGPPIPARCFDYE 273
Db 327 V-----KHLEQGGKFIMSYNHIQMEPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ 377
Qy 274 IEIREDDTTLTAVEN--ETYTLKTNETQLCFVVRKSVNIYCSDDGIHSEWSDKOCW 331
Db 378 VOYKKKSDSWEDSKTENLDRAHSMDLSOLEPDTSYCARVRVKPISNYDGIWSEYTW 437
Qy 332 EGEDLSKKTLLRFLWLPFGFILILVIFVTGLLL 363
Db 438 K-TDWVWPTL---WI-----VLILVFLILITLLL 461

Search completed: September 1, 2001, 19:16:24
Job time: 506 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:05:53 ; Search time 35.33 Seconds
(without alignments)
221.464 Million cell updates/sec

Title: US-09-077-817-2
Perfect score: 2104
Sequence: 1 MAFVCLAIGCLYTLISTTF.....LLLRKPNTPKMIPEFFCDT 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCBUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 2104 | 100.0 | 380 | 1 US-08-609-572-4 | Sequence 4, Appli |
| 2 | 2104 | 100.0 | 380 | 4 US-08-841-751-4 | Sequence 4, Appli |
| 3 | 2104 | 100.0 | 380 | 4 US-08-846-340-4 | Sequence 4, Appli |
| 4 | 1194.5 | 56.8 | 383 | 1 US-08-609-572-2 | Sequence 2, Appli |
| 5 | 1194.5 | 56.8 | 383 | 4 US-08-841-751-2 | Sequence 2, Appli |
| 6 | 1194.5 | 56.8 | 383 | 4 US-08-846-340-2 | Sequence 2, Appli |
| 7 | 311.5 | 14.8 | 420 | 1 US-07-757-390-13 | Sequence 13, Appl |
| 8 | 311.5 | 14.8 | 420 | 1 US-08-442-282-13 | Sequence 13, Appl |
| 9 | 311.5 | 14.8 | 420 | 1 US-08-442-281-13 | Sequence 13, Appl |
| 10 | 311.5 | 14.8 | 420 | 2 US-08-939-727-13 | Sequence 13, Appl |
| 11 | 310.5 | 14.8 | 396 | 1 US-07-757-390-14 | Sequence 14, Appl |
| 12 | 310.5 | 14.8 | 396 | 1 US-08-442-282-14 | Sequence 14, Appl |
| 13 | 310.5 | 14.8 | 396 | 1 US-08-442-281-14 | Sequence 14, Appl |
| 14 | 310.5 | 14.8 | 396 | 2 US-08-939-727-14 | Sequence 14, Appl |
| 15 | 295.5 | 14.0 | 427 | 4 US-08-969-125-9 | Sequence 9, Appli |
| 16 | 293 | 13.9 | 313 | 3 US-08-836-561-106 | Sequence 106, App |
| 17 | 292 | 13.9 | 335 | 1 US-07-947-130-2 | Sequence 2, Appli |
| 18 | 292 | 13.9 | 335 | 1 US-08-421-822-2 | Sequence 2, Appli |
| 19 | 292 | 13.9 | 335 | 1 US-08-421-823-2 | Sequence 2, Appli |
| 20 | 247 | 11.7 | 398 | 1 US-07-757-390-6 | Sequence 6, Appli |
| 21 | 247 | 11.7 | 398 | 1 US-08-442-282-6 | Sequence 6, Appli |
| 22 | 247 | 11.7 | 398 | 1 US-08-442-281-6 | Sequence 6, Appli |
| 23 | 247 | 11.7 | 398 | 2 US-08-939-727-6 | Sequence 6, Appli |
| 24 | 247 | 11.7 | 415 | 1 US-07-757-390-5 | Sequence 5, Appli |
| 25 | 247 | 11.7 | 415 | 1 US-08-442-282-5 | Sequence 5, Appli |
| 26 | 247 | 11.7 | 415 | 1 US-08-442-281-5 | Sequence 5, Appli |
| 27 | 247 | 11.7 | 415 | 2 US-08-939-727-5 | Sequence 5, Appli |

Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 69, Appli
Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-609-572-4

Query Match 100.0%; Score 2104; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.2e-208;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTTFGTSSTDEIKVNPQDFEIVDPGVLGYLYLQWQPLSLD 60

Db 1 MAFVCLAIGCLYTELSTTGTCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSKPKGIGVLLDTNLYNLFYWEGLDH 180
Db 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSKPKGIGVLLDTNLYNLFYWEGLDH 180
Qy 181 ALQCVDYIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Db 181 ALQCVDYIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Qy 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVENEYTYLKTINE 300
Db 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVENEYTYLKTINE 300
Qy 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLSKTLRLFWLPGFLLILVIFVTG 360
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLSKTLRLFWLPGFLLILVIFVTG 360
Qy 361 LLLRKPNTYPRKMIPEFFCDT 380
Db 361 LLLRKPNTYPRKMIPEFFCDT 380

RESULT 2

US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Bridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-841-751-4
Query Match 100.0%; Score 2104; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.2e-208;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIGCLYTELSTTGTCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTELSTTGTCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSKPKGIGVLLDTNLYNLFYWEGLDH 180
Db 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSKPKGIGVLLDTNLYNLFYWEGLDH 180
Qy 181 ALQCVDYIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Db 181 ALQCVDYIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Qy 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVENEYTYLKTINE 300
Db 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVENEYTYLKTINE 300
Qy 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLSKTLRLFWLPGFLLILVIFVTG 360
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLSKTLRLFWLPGFLLILVIFVTG 360
Qy 361 LLLRKPNTYPRKMIPEFFCDT 380
Db 361 LLLRKPNTYPRKMIPEFFCDT 380

RESULT 3

US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Bridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

Query Match 100.0%; Score 2104; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.2e-208;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAFVCLAGLCYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPLSLD 60
DB 1 MAFVCLAGLCYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPLSLD 60
QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
DB 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
DB 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
QY 181 ALOCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240
DB 181 ALOCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240
QY 241 PVLFTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLTKTTNE 300
DB 241 PVLFTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLTKTTNE 300
QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTLRLFWLPGFGLILVIFVTG 360
DB 301 TRQLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTLRLFWLPGFGLILVIFVTG 360
QY 361 LLRKPNTPYKMIPEFFCDT 380
DB 361 LLRKPNTPYKMIPEFFCDT 380
```

RESULT 4
US-08-572-2
Sequence 2, Application US/08609572
Patent No. 5710023
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-572-2

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Query Match 56.8%; Score 1194.5; DB 1; Length 383;  
Best Local Similarity 58.9%; Pred. No. 1.4e-114;  
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;  
QY 1 MAFVCLAGLCYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPLSLD 60  
DB 1 MAFV--HRCCLFLLCTITGYS----LEIKVNPQDFEILDGCLLGYLYLOWAPPVVIE 54  
QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120  
DB 55 KFKGCTLEYELKYRNVDSDSKWTIIITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114  
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180  
DB 115 SPWTEASYGISDEGSLETKIQDMKCIYNNWQYLLCSWKPGKTVYSDNTYTMFFWYEGLDH 174  
QY 181 ALOCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240  
DB 175 ALQCADYIQHDERKNGVCKLSNLDSSDKDFYICVNGSKLEPIRSSYTVFOLQNIKPLP 234  
QY 241 PVLFTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLTKTTNE 300  
DB 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLKRANE 294  
QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTLRLFWLPGFGLILVIFVTG 360  
DB 295 SEDLCFFVRCKVNIYCADGDIWSEWSEECWEGYTGPDSKII-FIVVPVCLFFTFLLLLLC 353  
QY 361 LLRKPNTPYKMIPEFFCDT 372  
DB 354 LIVEKEPEPTIL 365
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RESULT 5
US-08-841-751-2
Sequence 2, Application US/08841751
Patent No. 6214559
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/841,751

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/609,572

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: GI5268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-841-751-2

Query Match 56.8%; Score 1194.5; DB 4; Length 383;

Best Local Similarity 58.9%; Pred. No. 1.4e-114;

Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLAIGCLYTLSTTFCGTSSTTEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60

DB 1 MAFV--HIRCLCFILLCITIGYS----LEIKVNPQDFEILDPLGLLYLYLQWPPPVVIE 54

QY 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120

DB 55 KFKGCTLEYELKYNVDSDSWKTIITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180

DB 115 SPWIEASYGIDSEGSLETKIQDMKCIYNNQYLLCSWKPGITVSDNTYMTFFWYEGLDH 174

QY 181 ALOCVDYIKADQONIGCRFPYLPASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240

DB 175 ALOCADYLQHDKNVGVCKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTVFOLQNIKPLP 234

QY 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLKTTNE 300

DB 235 PEFLLHSIVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294

QY 301 TROLCFVVRKVNLYCSDGDIWSEWSKQWEGEDLSKTKTLRLFWLPFGFILLIVFTVG 360

DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDSKII-FIVPVCLEFFIFLLLLLC 353

QY 361 LLRLKPNYTPKM 372

DB 354 LIVEKEPEPTL 365

RESULT 6

US-08-846-340-2

Sequence 2, Application US/08846340

Patent No. 6248714

GENERAL INFORMATION:

APPLICANT: Collins, Mary

APPLICANT: Donaldson, Debra

APPLICANT: Fitz, Lori

APPLICANT: Neben, Tamlyn

APPLICANT: Whitters, Matthew

APPLICANT: Wood, Clive

TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/846,340

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/609,572

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: GI5268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-846-340-2

Query Match 56.8%; Score 1194.5; DB 4; Length 383;

Best Local Similarity 58.9%; Pred. No. 1.4e-114;

Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLAIGCLYTLSTTFCGTSSTTEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60

DB 1 MAFV--HIRCLCFILLCITIGYS----LEIKVNPQDFEILDPLGLLYLYLQWPPPVVIE 54

QY 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120

DB 55 KFKGCTLEYELKYNVDSDSWKTIITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180

DB 115 SPWIEASYGIDSEGSLETKIQDMKCIYNNQYLLCSWKPGITVSDNTYMTFFWYEGLDH 174

QY 181 ALOCVDYIKADQONIGCRFPYLPASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240

DB 175 ALOCADYLQHDKNVGVCKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTVFOLQNIKPLP 234

QY 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLKTTNE 300

DB 235 PEFLLHSIVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294

QY 301 TROLCFVVRKVNLYCSDGDIWSEWSKQWEGEDLSKTKTLRLFWLPFGFILLIVFTVG 360

DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDSKII-FIVPVCLEFFIFLLLLLC 353

QY 361 LLRLKPNYTPKM 372

DB 354 LIVEKEPEPTL 365

RESULT 7

US-07-757-390-13

Sequence 13, Application US/07757390

Patent No. 5453491

GENERAL INFORMATION:

APPLICANT: Takatsu, Kiyoshi

APPLICANT: Tomimaga, Akira

APPLICANT: Takagi, Satoshi

APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-757-390-13

Query Match 14.8%; Score 311.5; DB 1; Length 420;
Best Local Similarity 26.9%; Pred. No. 1e-23;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

Qy 27 DTEIKVNPQDFEIVDPGYLYLQWQPPLSLDFHFKECTVEYELKYRNIGSETWTKITIT 86
Db 25 DEKISLLPPVNFITKVVG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82

Qy 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKVODMDCV 146
Db 83 ES---KCVTLHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTGVNLTCT 135

Qy 147 -----YNNQYLL-CSWKPGIGVLLDPTNLYF---WYEGLDHALQCVDYIKAD 191
Db 136 TTTTNDYSLRYSQVSLHCTWLVTGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189

Qy 192 -GQNICRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRIACWFFRTFLSKGRDLAVLVNGSSKHSARFPDQLFALHAIDQINPLNVTAEI 249

Qy 249 ESSCEIKLWSIPLGPAPRCDFYEIREDDTTLVATVENETTYLTKTNETRQLCFVV 308
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIKHNTRNGYLQIEKLTNAFISIIDLSKYDVQV 308

Qy 309 RSKVNIYCSDDGIWSESDKOCWEGEDLSKTLRLFWLPGFILL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHP--LREW----FVIVIMATICFILLISLI 361

Qy 363 LRKNTTPKMP 374
Db 362 CKICHLWIKLFP 373

RESULT 8
US-08-442-282-13
; Sequence 13, Application US/08442282

Patent No. 5760204
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomiaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-442-282-13

Query Match 14.8%; Score 311.5; DB 1; Length 420;
Best Local Similarity 26.9%; Pred. No. 1e-23;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

Qy 27 DTEIKVNPQDFEIVDPGYLYLQWQPPLSLDFHFKECTVEYELKYRNIGSETWTKITIT 86
Db 25 DEKISLLPPVNFITKVVG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82

Qy 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKVODMDCV 146
Db 83 ES---KCVTLHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTGVNLTCT 135

Qy 147 -----YNNQYLL-CSWKPGIGVLLDPTNLYF---WYEGLDHALQCVDYIKAD 191
Db 136 TTTTNDYSLRYSQVSLHCTWLVTGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189

Qy 192 -GQNICRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRIACWFFRTFLSKGRDLAVLVNGSSKHSARFPDQLFALHAIDQINPLNVTAEI 249

Qy 249 ESSCEIKLWSIPLGPAPRCDFYEIREDDTTLVATVENETTYLTKTNETRQLCFVV 308
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIKHNTRNGYLQIEKLTNAFISIIDLSKYDVQV 308

Qy 309 RSKVNIYCSDDGIWSESDKOCWEGEDLSKTLRLFWLPGFILL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHP--LREW----FVIVIMATICFILLISLI 361

QY 363 LRKPNTPKMP 374
Db 362 CKICHLWIKLFP 373

RESULT 9

US-08-442-281-13
; Sequence 13, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-13

Query Match 14.8%; Score 311.5; DB 1; Length 420;
Best Local Similarity 26.9%; Pred. No. 1e-23;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPDPDFVDPGILGYLYLQWQPLSLDHFKECTVEYELKYRNIGSETWTKIT 86
Db 25 DEKISLPPVNFNTIKVTG-LAQVLLQWKPNPQDEQ-RNVNLEYQVKINAPKEDDYETRIT 82
QY 87 KNLHYKDFDLNKGIEAKIHTLLPWOCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
Db 83 ES---KCVTILHKFGSAVSRTILQ---NDHSLSSWASAEHLH-APGSPGTSVNLCT 135
QY 147 -----YNNQYLL-CSWPGIGVLDTNVLNLEY-----WYGLDHALQCVDYIKAD 191
Db 136 TMTEDNYSRLRSQVSLHCTWLVTGTDAPEDTQYFLYIRYGSWTE-----ECQYSKDT 189
QY 192 -GONIGREFP--YLEASDYKDFICVNGSSSENKPIRSSYFTFQLOINIVKPLPPVYLTFTR 248
Db 190 LGRNIACWFFRTFILSGROWLAVLVNGSSKSHSAIRPFDQIFALHAIQINPLNVTAEI 249

QY 249 ESCEIKLKWISPLGPICPARCFDEYIEIREDDTTLVTATVENETYYTLTKTNETRQLCFV 308
Db 250 EGT-RLSIQNEKPVSAPIHCDFEYVHNRNGYLOIEKLMTNAPISIIDDLUSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWSKOCWEGEDLSKTKLLRFLWLPFGFILIL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREN---FVIVIMATCIFILLISLSI 361
QY 363 LRKPNTPKMP 374
Db 362 CKICHLWIKLFP 373

RESULT 10

US-08-939-727-13
; Sequence 13, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-939-727-13

Query Match 14.8%; Score 311.5; DB 2; Length 420;
Best Local Similarity 26.9%; Pred. No. 1e-23;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPDPDFVDPGILGYLYLQWQPLSLDHFKECTVEYELKYRNIGSETWTKIT 86
Db 25 DEKISLPPVNFNTIKVTG-LAQVLLQWKPNPQDEQ-RNVNLEYQVKINAPKEDDYETRIT 82
QY 87 KNLHYKDFDLNKGIEAKIHTLLPWOCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
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| Db | 83 | ES--KCVTILHRGFSASVTIIQ--NDRSLASSWASAEHLH-APPGSPGTISVINTJCT | 139 |
| Qy | 147 | -----YYNQVYLL-CSWKPGIGVLLDTWNIFY----WYEGLDHALQCVDYIKAD | 191 |
| Db | 136 | TNTTETDNYSLRYSQVSLHCTWLVTGDPADETOYFLYRYGSWTE-----EQEYISKDT | 189 |
| Qy | 192 | -GNIGCRFP--YLEASDYKDFICYVNGSSGENKPIRSSYFTFQLONTVKKPLPYYLFTFR | 248 |
| Db | 190 | LGRNIACWFPRTILSKGRDWLAVLVNGSSKSHAIRPDFQLFALHAIDQINPPLNVTAEI | 249 |
| Qy | 249 | ESSEIKLKWISIPLGPIPARCFPYETIEIRDDTTLVTATVENETYTLTKTNTNEHROLCFVV | 308 |
| Db | 250 | EGT-RUSIQEKQKPVSAFFPHCFDYEVIKHITRNGYIQIEKLMTNAPFISIIDDLISKYDVQV | 308 |
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| Db | 309 | RAAVSSMCREAGLWSEWS-OPIVVGNDHEKPP--LREW----FVIVMATICFILLISLI | 361 |

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-14

Query Match          14.8%; Score 310.5; DB 1; Length 396;
Best Local Similarity 26.6%; Pred. No. 1.2e-23;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDFEIVDPCYLGVLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIIIT 86
DB 25 DEKISLLPPVNTIKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
QY 87 KNLHYKDGFDLKNKGIEAKIHLLPWQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSPGTSIVNLCT 135
QY 147 -----YNNQYLL-CSWKEGIGVLLDTNINLFY---WYEGLDHALQCVDIYKAD 191
DB 136 TMTEDNYSRLRSQVSLHCTWLVGTDAPEDTQFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQNLQIVKPLPPVLTFT 248
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QY 363 LRKPNTPYKMP 374
DB 362 CKICHLWIKLEP 373

RESULT 13
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-14

Query Match          14.8%; Score 310.5; DB 1; Length 396;
Best Local Similarity 26.6%; Pred. No. 1.2e-23;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDFEIVDPCYLGVLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIIIT 86
DB 25 DEKISLLPPVNTIKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
QY 87 KNLHYKDGFDLKNKGIEAKIHLLPWQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSPGTSIVNLCT 135
QY 147 -----YNNQYLL-CSWKEGIGVLLDTNINLFY---WYEGLDHALQCVDIYKAD 191
DB 136 TMTEDNYSRLRSQVSLHCTWLVGTDAPEDTQFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQNLQIVKPLPPVLTFT 248
DB 190 LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSATRPDQFLFALHAIQINPPLNVTAEI 249
QY 249 ESSCEIKLKWISPIGPIPARCFDYEIEIREDDTTLVTATVENETTYTLKTTNETRQLCFV 308
DB 250 EGT-RLSQWEKPVSAFPIHCFDYEIVKIHNRNGYLQIEKLTNAFTSIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESDKOCWEGEDLSKTKTLRFLWLPFGFILL-----VIFVTGLL 362
DB 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATIFILLISLI 361
QY 363 LRKPNTPYKMP 374
DB 362 CKICHLWIKLEP 373

RESULT 14
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
```

NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-939-727-14

Query Match 14.8%; Score 310.5; DB 2; Length 396;
Best Local Similarity 26.6%; Pred. No. 1.2e-23;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVPPDQFEIVDPCYGLYLQWQPPSLDHFKECTVEYELKYRNIGSETWTKTIIT 86
Db 25 DEKISLLPPVNTTKVKG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDIYETRI 82
QY 87 KNLHYKDGFDLNGKIEAKIHTLPPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
Db 83 ES---KCVTLHKFGSASVRILO--NDHSLASSWASAEHL-APGSPGTSIVNLCT 135
QY 147 -----YYNQYLL-CSWKGIGVLLDTNLYFY----WYEGLDHALQCVDYIKAD 191
Db 136 TTTTNDYSLRSYQVSLHCTWLVGTDAPEDTQFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQLOINVKPLPPVLIATR 248
Db 190 LGRNIACWPTFTLSKGRDVLAVNGSSKHSAIRPFDQALHAIDQINPPLNVTAEI 249
QY 249 ESSGEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFV 308
Db 250 EGT-RLSTQWEKPVSAFPIHCFDYEIVKHTNRNGYLQIEKLMTNAFISIIDLSKYDVQV 308
QY 309 RSKYNYCSDGISEWSDKOCWGEDLSKTKTLRFLWLPFGFIL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI 361
QY 363 LRKPNTPKMP 374
Db 362 CKICHLWIKLPP 373

RESULT 15
US-08-969-125-9
Sequence 9, Application US/08969125B
Patent No. 6143871
GENERAL INFORMATION:
APPLICANT: BONNEFOY, JEAN-YVES
GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,125B

FILING DATE: 12-No. 6143871-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 14.08%; Score 295.5; DB 4; Length 427;
Best Local Similarity 26.0%; Pred. No. 4.7e-22;
Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 11 LYTFLLISTFEGCTSSDTEIKVNPQDFEIVDPCYGLYLQWQPPSLDHFKECTVEY- 69
Db 10 LWALLCAGGGGGGGAAPTETQPVNLSVSVENLCTVITWNPPEGAS--SNCSLWYF 67
QY 70 ---ELKYRNIGSETWTKTIITKNLHYKDGFDLNGKIEAKIHTLPPWQ--TNGSEVQSSWA 124
Db 68 SHFGDKQDKKIAPTERRSI-----EVLNERICLQVGS---QCSTNESEKPSILV 114
QY 125 ETTTWIS--PQGIPTKVQDMDCVYNNQYLLCSWKGIGVLLDTNLYFYEGLDHALQ 183
Db 115 EKC--ISPEGDPEASVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYWHRSLKTHQ 172
QY 184 CVDYIKADGQNGICRFPYLEASD--YKDFYICVNGSSSENKPIRSYFTFQLOINVKPLPP 241
Db 173 C-ENIFREGQYFGCSFDLTQVKSFEQHSQVQIMVKDNAGKIKPSFNIVPLTSRVKPPDP 231
QY 242 --VYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDT-----LVTATVENETY 293
Db 232 HIKNLSFHND--DLVQWENPQFI-SRCLFYEVEVNNSTETHNVFYVQEAECENPEF 287
QY 294 TLKTTNETRQLCFV-----RSKVNICY-SDDGIWSEWSKOCWGEDLSKK 339
Db 288 ERNVENTS---CFMVPQVLPDTLNTVIRVIRVTKNLCLYEDDKLWSNWSQEM-----SIGKK 339
QY 340 TLLRFWLPF-----GFILILVIFVTGL--LLRKPNTP-KMIPFEFFCD 379
Db 340 RNSTLYITMLLIVPVIAGAIIVLLLLYLRKLIIFPPIPDGPKIFKEMFGD 391

Search completed: September 1, 2001, 19:08:35
Job time: 162 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:54 ; Search time 15.95 Seconds
(without alignments)
1805.265 Million cell updates/sec

Title: us-09-077-817-12
Perfect score: 2087
Sequence: 1 MAFVCLAIGCLYFLISTTF.....TGILLRKPNTYPKMVRVTL 378
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 310.5 | 14.9 | 420 | 2 S21052 | interleukin-5 rece |
| 2 | 292 | 14.0 | 335 | 2 A40267 | interleukin-5 rece |
| 3 | 261 | 12.5 | 831 | 2 J01655 | prolactin receptor |
| 4 | 241 | 11.5 | 415 | 2 S12357 | interleukin-5 rece |
| 5 | 220 | 10.5 | 369 | 2 A42365 | interleukin-2 rece |
| 6 | 216.5 | 10.4 | 830 | 2 I50455 | prolactin receptor |
| 7 | 212.5 | 10.2 | 369 | 2 I49280 | interleukin-2 rece |
| 8 | 208 | 10.0 | 373 | 2 A55718 | interleukin-2 rece |
| 9 | 195 | 9.3 | 878 | 1 A40091 | interleukin-3 rece |
| 10 | 180.5 | 8.6 | 897 | 1 A39255 | cytokine receptor |
| 11 | 178 | 8.5 | 896 | 2 I56363 | interleukin-3 rece |
| 12 | 173.5 | 8.3 | 896 | 1 A35782 | cytokine receptor |
| 13 | 167 | 8.0 | 581 | 2 I45971 | prolactin receptor |
| 14 | 166 | 8.0 | 310 | 2 A29884 | prolactin receptor |
| 15 | 166 | 8.0 | 412 | 2 A41070 | prolactin receptor |
| 16 | 166 | 8.0 | 610 | 2 A36116 | prolactin receptor |
| 17 | 165 | 7.9 | 610 | 2 A34631 | prolactin receptor |
| 18 | 159 | 7.6 | 292 | 2 I77525 | lactogen receptor |
| 19 | 159 | 7.6 | 303 | 2 I77524 | prolactin receptor |
| 20 | 159 | 7.6 | 608 | 2 I53269 | prolactin receptor |
| 21 | 153 | 7.3 | 616 | 2 A30304 | prolactin receptor |
| 22 | 151 | 7.2 | 622 | 2 A40144 | prolactin receptor |
| 23 | 150.5 | 7.2 | 917 | 2 I49699 | prolactin receptor |
| 24 | 142.5 | 6.8 | 400 | 2 S06945 | granulocyte-macrop |
| 25 | 138 | 6.6 | 378 | 2 A40266 | interleukin-3 rece |
| 26 | 134.5 | 6.4 | 1097 | 2 S17308 | leukemia inhibitor |
| 27 | 133.5 | 6.4 | 333 | 2 S13684 | granulocyte-macrop |
| 28 | 133.5 | 6.4 | 378 | 2 S50040 | granulocyte-macrop |
| 29 | 131.5 | 6.3 | 630 | 2 I51086 | prolactin receptor |

ALIGNMENTS

RESULT 1

S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_Change 01-Dec-2000
C;Accession: S21052; S21053; A46175; S78106; S78107
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor.
A;Reference number: S21050; MUID:92121815
A;Accession: S21052
A;Molecule type: DNA
A;Residues: 1-420 <MUR>
A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A;Experimental source: clone lambda h5R.12
A;Accession: S21050
A;Molecule type: DNA
A;Residues: 1-395, 'I' <MU2>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A;Experimental source: clone lambda h5R.27
A;Accession: S21053
A;Molecule type: mRNA
A;Residues: 1-332, 'K' <MU3>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A;Experimental source: clone lambda h5R.25
R;Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum
A;Reference number: A46175; MUID:92357767
A;Accession: A46175
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 333-420 <TAV>
A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R;Murata, Y.
submitted to the EMBL Data Library, July 1991
A;Reference number: S78106
A;Accession: S78106
A;Molecule type: DNA
A;Residues: 1-128, 'I', 130-395, 'I' <MUW>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R;Murata, Y.
submitted to the EMBL Data Library, September 1991
A;Reference number: S78107
A;Accession: S78107
A;Molecule type: mRNA
A;Residues: 1-128, 'I', 130-332, 'K' <MU4>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

F:345-365/Domain: transmembrane #status predicted <TM>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 310.5; DB 2; Length 420;
Best Local Similarity 27.9%; Pred. No. 3.5e-17;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

```
QY 27 DTEIKVNPQDFEIVDPGGLYLYLQWQPPSLDHFRECTVEYELKYNIGSETWKTIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPPVFTIKVTG-LAQVLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKDGFLNKIGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSASVRILO---NDHSLASSWASAEHL-APGSPGTSVNLNCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNINLFY----WYEGLDHALQCVDIKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTNDYNSRLRSYQVSLHCTWLVTGTDAPETQYFLYRYGSWTE-----ECOYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLNIVKPLPPVLTFT 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPRTFILSKGRDLWLVNGSSKHSAIRPDFQALHAIDQINPPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVTATVENETITLKTNETRQLCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYKIHNRNGYLOIEKLTNAFISIIDLSKYDVQV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 RSKYNIYCSDDGIWSEWSDKOCWGEDLSKTLIRFWLPFGFILLIVFTVGLLL 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RAAVSSMCREAGLWSEWS-QPIYGVNDEHKP--LREW---FVIVIMATICIFILL 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 2
A:040267
Interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuytens, T.; Van der Heyden, J.; Fiers, W.; PL
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 14.0%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 7.8e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

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QY 27 DTEIKVNPQDFEIVDPGGLYLYLQWQPPSLDHFRECTVEYELKYNIGSETWKTIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPPVFTIKVTG-LAQVLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKDGFLNKIGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSASVRILO---NDHSLASSWASAEHL-APGSPGTSVNLNCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNINLFY----WYEGLDHALQCVDIKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTNDYNSRLRSYQVSLHCTWLVTGTDAPETQYFLYRYGSWTE-----ECOYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLNIVKPLPPVLTFT 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPRTFILSKGRDLWLVNGSSKHSAIRPDFQALHAIDQINPPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVTATVENETITLKTNETRQLCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYKIHNRNGYLOIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKYNIYCSDDGIWSEWS 326
 :
Db 309 RAAVSSMCREAGLWSEWS 326
 :
RESULT 3
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 186, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: Kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 12.5%; Score 261; DB 2; Length 831;
Best Local Similarity 26.3%; Pred. No. 7.3e-13;
Matches 98; Conservative 55; Mismatches 175; Indels 44; Gaps 16;

```
QY 18 TTFGCTSSSTEIKVN--PPQDFE---IVDPG-----YLGYLQWQPPLSL 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 TTFNITVATNEIGSNSDDQYVDVTSIVQGPSVNLTLTKRSANIMYLWAKWSPPLA 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 DHFKECTVEYELKYNIGSETWKTIITLKNHYKDGFLNKIGIEAKIHTLLPWQCTNGSEV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 DASSNHLHYELRIKPEKEEWETI---SVGVQTCQKINR-LNAGMRVYVQVRCITDPGE 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 QSSWAETTYWISPOG-IPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNINLFYWEGL 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 WSESSSEHILIPSGQSPPEKPTTIKRSPEKETFTCWKAPGLDGGHPTNTLLYSKEGE 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 DHALQCVDIKADGQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLNIVKP 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 EQVVECPDY-RTAGPN-SCVFDKKHTSFWTIYITVRATNEMGNSSDPHYVDVTYIVQP 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 LPPVLTFTRESCEIK-----LWS-IPLGPAPARCFDYEIEIR---EDDTTLVTATVEN 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 DPPVNVLTLELKPINRKPYLVLTWSPPLADVRSWGLTLEYELKPEGESEWETIFVQG 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 ET-YTLKTTTETROLCFWRSKVNIVCSDD--GIWSEWSKQWE-GEDLSKTLIRFWL 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 391 QTQYKMFSLNPKKYI-----IQHCKPDHGGSSSESNYIQIPNDFVKDMI-VWI 443
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 PFGFILLIVFV 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 444 VLGVLSLICLI 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 4
S12357
Interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S12357
R:Takaki, S.; Tominaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu
EMBO J. 9, 4367-4374, 1990

A>Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A;Reference number: S12357; MUID:91092260
A;Accession: S12357
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-415 <RA>
A;Cross-references: GB:090205; NID:g220465; PIDN:BAA14231.1; PID:g220466
C;Keywords: cytokine receptor; transmembrane protein

Query Match 11.5%; Score 241; DB 2; Length 415;
Best Local Similarity 24.9%; Pred. No. 1.2e-11;
Matches 80; Conservative 65; Mismatches 144; Indels 56; Gaps 17;
Qy 34 PPQDFEIVPGYGLYLQWOPPLSLDHFKECTVEYELKRNIGSETWKTITKLNHYKD 93
Db 29 PVNFTIKATG-LAQLVLLHWDPNPQEQ-RHVLDLHYHVKINAPQDEYDTRKTES---KC 83
Qy 94 GFDLNGKIEAKIHLLPWQCTNGSEVSSNAETTYWISPGIPETKVQDMDCVYVNWYL 149
Db 84 VTPLHEGFAASVRIK---SSHTTLASSWVSABL-KAPPGSPGTSVTNLCTTHTTVVSS 139
Qy 150 -----WQY-LLCSWKKPCIGVLLDTNLYNLFYWEGLDHALQCVDIK-ADQNGICRPP- 200
Db 140 HTHLRPVQVSLURCTWLVGKADAPDTQFLYRFGVLTE--KCQYSRDLNRTACWPPR 197
Qy 201 -YLEASDYKDFYICVNGSSENKPIRSSVFTFQLNIVKPLPPVYLTFTRESSCEIKLW 259
Db 198 TFINSKGEQLAVHNGSSKRAAKLPDQLESPLAIDQVNPVNTVEIESN-SLYTOWE 256
Qy 260 IPLGPPIPARCFDYIEIREDD-----TTLVATVENETTLTKTNETRQLCFV 308
Db 257 KPLSAFPHDPCFNYELKIYTNKNGHIQKEKLIANKFISKIDVDVSYIQ-----V 305
Qy 309 RSKYNIYVSDGCIHNSWSDKOCWGEDLSKTKTLRFW----LPGFILLIVIF 357
Db 306 RAAVSSPCMPGRGWS-QPIYVGKE--RKSLVE-WHLIVLPTAACFVLLIF 354

RESULT 5
A42565
Interleukin-2 receptor gamma chain - human
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
A;Accession: A42565; A46591; I54332
R;Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, N.; Tanaka, H.; Science 257, 379-382, 1992
A>Title: Cloning of the gamma chain of the human IL-2 receptor.
A;Reference number: A42565; MUID:92335883
A;Accession: A42565
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A;Residues: 1-369 <RA>
A;Cross-references: GB:D11086; NID:g303611; PIDN:BAA01857.1; PID:g219890
A;Experimental source: MOLT beta lymphoid cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109167)
R;Nozuchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J. J. Biol. Chem. 268, 13601-13608, 1993
A>Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A;Reference number: A46591; MUID:9233887
A;Accession: A46591
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-369 <RS>
A;Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058
R;Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993
A>Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked
A;Reference number: I54332; MUID:94004847
A;Accession: I54332
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-369 <RE2>

A;Cross-references: GB:L19546; NID:g349631; PIDN:AA37524.1; PID:g349632
C;Genetics:
A;Gene: GDB:IL2RG; SCIDX1; IMD4
A;Cross-references: GDB:134807; OMIM:308380
A;Map position: Xq13.1-Xq13.1
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A;Note: defects are associated with an X-linked form of severe combined immunodeficiency
C;Superfamily: Interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.5%; Score 220; DB 2; Length 369;
Best Local Similarity 25.5%; Pred. No. 4.7e-10;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;
Qy 97 LNKIEAKIHLLPWQCTNGSE-VQSSWAETTYWISPGIPETKVQDMDCVYVNWYL 155
Db 19 LGVGLNTILP-----PNGNEDTADFTLTSTLPLPEVQCFVFNVEYNNC 72
Qy 156 SW-----KPGIGVLLDTNLYNLFYWEGLD--ALQCVDIKADQNGICRFPYLEASDY 207
Db 73 TWSSEPPQ-----TNLTLYWYKNSDNDKVQKCSHYLSEITSGCQLQKKEIHL 125
Qy 208 KDFYICVNGSSENKPIRSSVFTFQLNIVKPLPPVYLTFTRESSCEIKLWISPLGPIPA 267
Db 126 QTFVVLQDPRE--PRQATQMLKQLNIVPAPENLTLHKLSELSQLELNN--NRFLN 180
Qy 268 RCFDYETEIREDD--DTTLVATVE-NEYTLTKTNETRQLCFVRSKYNVYSDGGINSEW 325
Db 181 HCLHVLQVYRTDWDHSTEQSVYRHKFSLPSVDGQKRYTFVRSRFPLCGSAQHSW 240
Qy 326 SDKQWGEDLSKTKTLRFWLPFGFILILVIFVTG 360
Db 241 SHPIHW-GSNTSKEN-----PFLFALEAVVISVG 268

RESULT 6
I50455
prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
A;Accession: I50455
R;Chen, X.; Horseman, N.D. Endocrinology 135, 269-276, 1994
A>Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor
A;Reference number: I50455; MUID:94283267
A;Accession: I50455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-830 <CHE>
A;Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C;Superfamily: cytokine receptor homology
F;36-220/Domain: cytokine receptor homology <CRS1>
F;240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.4%; Score 216.5; DB 2; Length 830;
Best Local Similarity 24.4%; Pred. No. 2.5e-09;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;
Qy 18 TTFGCTSSDTEIKVNPQDPFEIVDPGVILG-----YLYLQW 53
Db 97 TTYNTYVWAMNEIGSNSS-----DPQYVDVTSIVQDPVYNLSLETKTSASTYLLAKW 150
Qy 54 OPPLSLDHFKECTV-EYELKRYNIGSETWKTITKLNHYKDGFDLNGKIEAKIHLLPWQ 112
Db 151 SPPLPADVTNSHVRYELRLKPEKEWETV---SVGQYQYKYNR-LQAGVKYVQVR 206
Qy 113 CTNGSEVQSSWAETTYWISPOG-IPETKVQDMDCVYVNWYLLCSWKKPGICGILLDTN 171
Db 207 CVLDIGEWSEWSERHIIHPNGESPPKEPTTIKRSPEKETFTCWKPGSGGHPNTTL 266
Qy 172 FYWYEGLDHALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSVFTFQ 231

Db 267 LYSKEGGEVVECPDY-KTAGPN-SCYFDKKHTSFWIYNTVKTATNEIGSNVSDPLYVD 324
 Qy 232 LQNIIVKPLPPVLTFTRESSCEIK-----LKWS-ITLGPPIPA--RCFYDEIETIREDDTTLV 284
 Db 325 VTYIVQTDVNTVLTLEKLTNNRPYLVLTWSPPLADVRSGWLTLDYELRLKPEEA--- 381
 Qy 285 TATVENETITLKTNETRQLCFVY---RSKNVIYCSDD--GIWSEWS-DKQCWEGEDLS 337
 Db 382 -----EEWETTFVQOQTHYKMFSLNPGKYIVQIHCPDHHGSEWSLEKYLQIPTDFR 436
 Qy 338 KKTLLRFWLPFGFLLILVIFV 358
 Db 437 IKDMV-VMIIVGVLSLILCV 456

RESULT 7
 149280
 Interleukin-2 receptor gamma chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
 R:Caio, X.; Kozak, C.A.; Liu, Y.
 Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
 A>Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gene
 A:Reference number: A47514; MUID:93391374
 A:Accession: I49280
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <KAO>
 A:CROSS-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350
 A:Accession: A47514
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-369 <RE2>
 A:CROSS-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
 Biochem. Biophys. Res. Commun. 193, 356-363, 1993
 A>Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of function
 A:Reference number: JN0592; MUID:93277575
 A:Accession: JN0592
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-369 <KUM>
 A:CROSS-references: DBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
 R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
 Gene 130, 303-304, 1993
 A>Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
 A:Reference number: JN0775; MUID:93366191
 A:Accession: JN0775
 A:Molecule type: mRNA
 A:Residues: 1-369 <KOB>
 A:CROSS-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
 R:Chiu, R.K.; Dougherty, G.J.
 submitted to the EMBL Data Library, October 1993
 A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
 A:Reference number: S37582
 A:Accession: S37582
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
 R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
 Eur. J. Immunol. 24, 3014-3018, 1994
 A>Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal location
 A:Reference number: I53398; MUID:95104285
 A:Accession: I53398
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <RES>
 A:CROSS-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
 C:Genetics:
 A:Gene: IL-2Rgamma

A: Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
 C: Complex: The high affinity receptor is a heterotrimer of alpha (see PIR-UHMS2), beta
 eptors.
 A: Description: receptor for interleukin-2
 A: Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
 C: Superfamily: interleukin-2 receptor gamma chain
 C: Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
 F: 1-22/Domain: signal sequence #status predicted <SIG>
 F: 23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
 F: 256-284/Domain: transmembrane #status predicted <TMN>
 F: 71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 10.2%; Score 212.5; DB 2; Length 369;
 Best Local Similarity 26.9%; Pred. No. 1.9e-09;
 Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

Qy 136 PETKVQDMDCVYNNQYLLCSW----KPGIGVLLDTNNLFYWEGLDHAL--OCVDYIK 189
 Db 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPPQA-----TNLTLYRYKVSNDWTFQCSHYLF 107
 Qy 190 ADGONICGRFPYLEADYKDFYICVNGSSSENKPIRSYFTFQLONIYKPLPPVYLTFRE 249
 Db 108 SKEITSGCQIKEDIQLYQTFVVL--ODPOKQORRAVQKLNLQNLVIRAPENLTLSNL 165
 Qy 250 SSCEIKLKWSITPLGPPIARCFDEYIEIREDDTLVLTATVENE--TYTLKTNETRQLCFV 307
 Db 166 SESOLELRWK--SRHIKERCLQYLVQYRSNDRSRTWELIVNHEPRFSLPSVDEULKRYTFR 223
 Qy 308 VRSKVNICYSDDDGIWSEWSKQWEG-----EDLSKTKLLRFWLPFGF--ILILVIFVTGL 361
 Db 224 VRSRYNICSSQQWKSQPVHWSHTVEENPSLFALEAVLIPVGTMLITLIFVYCW 283
 Qy 362 LLRKPNTYP 370
 Db 284 LERMPPIPP 292

RESULT 8
 A55718
 Interleukin-2 receptor gamma chain precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
 C:Accession: A55718
 R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
 Genomics 23, 69-74, 1994
 A>Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combi
 A:Reference number: A55718; MUID:95130114
 A:Accession: A55718
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-373 <HEN>
 A:CROSS-references: GB:U04361; NID:g517411; PIDN:AAC48403.1; PID:g517412
 C: Superfamily: interleukin-2 receptor gamma chain
 C: Keywords: cytokine receptor; duplication

Query Match 10.0%; Score 208; DB 2; Length 373;
 Best Local Similarity 26.0%; Pred. No. 4.3e-09;
 Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

Qy 115 NGSE-----VQSSWAETTYWISPOGIPETKYQDMDCVYNNQYLLCSW-----KPGI 161
 Db 31 NGNEDITPDPFLFATPSET---LSVSSLPLPEVO---CFVFNVEYMNCTWNSSEPPR-- 82
 Qy 162 GVLLDTNLYNLYWYEGF--DHALQCVDYIKADGONICGRFPYLEADYKDFYICVNGSS 219
 Db 83 -----TNLTLYRYKVSNDKQVCEGHYLFSEVTACWKLQKEIHLXYTFVQLRDPRE 137
 Qy 220 NKPIRSYFTFQLONIYKPLPPVYLTFRESSCEIKLWSIPLGPIPARCFDEYIEIREDD 279
 Db 138 --PRQSTQKLQNLVIRAPENLTLSNLSEQLSLSW---NRHLDHCLGHEHVQVRS 192

RESULT 10
A39255
cytokine receptor common beta chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C:Accession: A39255
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-
A:Reference number: A39255; MUID:91088571
A:Accession: A39255
A:Molecule type: mRNA
A:Residues: 1-897 <HAY>
A:Cross-references: GB:M30275
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C:Genetics:
A:Gene: GDB:CSF2RB
A:Cross-references: GDB:126838; OMIM:138981
A:Map position: 22q13.1-22q13.1
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-897/Product: cytokine receptor common beta chain #status predicted <MAT>
F:17-443/Domain: extracellular #status predicted <EXT>
F:35-332/Domain: cytokine receptor homology <CRS1>
F:250-431/Domain: cytokine receptor homology <CRS2>
F:444-460/Domain: transmembrane #status predicted <TMN>
F:461-897/Domain: intracellular #status predicted <INT>

Query Match 8.6%; Score 180.5; DB 1; Length 897;
Best Local Similarity 22.6%; Pred. No. 2e-06;
Matches 90; Conservative 58; Mismatches 146; Indels 105; Gaps 21;

QY 32 VNPQDFEIVDPGLGY-----LYLQWQP-----LSLDHF----- 62
DB 97 VPCQSFVWTDVDFGQDPRLGLTRVTLTQHVQPEPRDLQISTDQDHFLLTWSVAL 156
QY 63 -----KCTVEYELKYRNGSETWK--TIITKNLHYKDGFDLNGIE-----A 103
DB 157 GSPQSHWLSGDLFEVYKRL-QDSHEDAAILLSNTS-----QATLGPHELMPSSTYYA 210
QY 104 KIHT-LLPMQCTNGSEVQSSWAETTYWISPGIPETKVQDMDCVYNNQVLLCSWKPGIG 162
DB 211 RVRTLAPGSRLSGR--PSKWSPEVCWDSQPG-DEAQPQNLCEFFDCAAVLSCSWEVRKE 267
QY 163 VLLDTYNLYFWTEGLDHALQCDVYIKADQNIG-----CRFPYLEADYKDFYICVN 215
DB 268 VASSVFGFLFYKFPSPDAGEECSPVLV---EGLSLHTRHHCQIPVPDPATHGQYIVSVQ 324
QY 216 GSSENKPIRSYFTFQNLQTVKPLPPVYLFTRESSCEIKLKWISPLGPIPARCFDYEIE 275
DB 325 PRAEKHIKSSV-----NI--QMAPPSLNVTKGD--SYSLRWETMKRVEHIDHTEIQ 375
QY 276 IREDDTLTVAT-VENETYTLKTN-----ETRLQCFV-VRSKNVIYCSDDGIWE 324
DB 376 YRKD----TATWKDSKTETLQNAHSMALPALEPSTRYWARVRVTRSTCY---NGIWE 427
QY 325 WSDKQWGEEDLSKYLRLRWLPFGFILLIVFTGLLL 363
DB 428 WSEARSWDTESV-----LPMWVLALIVIFLTAVL 457

RESULT 11
I56563
interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia
A:Reference number: I56563; MUID:95370942

A;Accession: I56563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-896 <RES>
A;Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C;Genetics:
A;Gene: r1l-3beta
C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C;Keywords: cytokine receptor
F;39-235/Domain: cytokine receptor homology <CRS1>
F;253-433/Domain: cytokine receptor homology <CRS2>

Query Match 8.5%; Score 178; DB 2; Length 896;
Best Local Similarity 21.4%; Pred. No. 3.2e-06;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLATGCL--YT-FLISTTFTGCTSSDTEIKVN-----PPQDFEIVDPGVLGYL 49
DB 94 CVPRRCVLPYTFQSVSKEDYYSLOQDRDLSHLVPLAQHVQPPPKDISISPSG--DHF 151
QY 50 YLQWQPLP---SLDHFKECTVEYELKYNIGSETWKTITKLNHYKDGFDLNGKIEAKIH 106
DB 152 LKWSVPLGDAQVLSLQSDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLPEK 203
QY 107 TLPL-----WQCTNGSEVQ---SSWAETTYWISPGIPETKQVDMDCVYNNWVLL 154
DB 204 LFLPNSIVARVRAQLPGSSLSGRPSGMSPEVHWDSETE-DKARPQNLCQFFDGIQSLN 262
QY 155 CSWAPGIGVLLDTNLYNFWYEGLDHALQVDYIKADGQNTGCRFPYLEASDYKDFYICV 214
DB 263 CSWEVWTRVTDVSFGLFYSSPKAGEKKSPVVK-----LQASRYTRYHCSL 311
QY 215 NGSENKPIRSSYFTFOLQ-----NIVKPLP-VYLTFTRESSCEIKLKWISPL 262
DB 312 NVSD---PAHSQYTVSVKRLQEQKFIESFNHIOQNPPTLNLTKNRDS---YSLHWETQK 365
QY 263 GPIPARCFDYIEIR-----EDDTTLVTATVENETTYTLTKTNETRQICFVVRKSVNIYC 316
DB 366 MSYPIQHAFOVQYKKLDRWEDSKT---ENLNHNSMDLPQLEPGTSYCARVRVKTIP 421
QY 317 SDDGIWSEWSKQWEGDLSKTKLLRFLWLPFGFILVIVFTVGLL 363
DB 422 EYKGLWSEWSNECTWT-TDWVMPPL---WI-----VLILVFLILTLFL 460

RESULT 12
A35782
cytokine receptor common beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A35782
R;Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A;Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein
A;Reference number: A35782; MUID:90319131
A;Accession: A35782
A;Molecule type: mRNA
A;Residues: 1-896 <GOR>
A;Cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C;Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptors
C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C;Keywords: cytokine receptor; duplication; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F;23-441/Domain: extracellular #status predicted <EXT>
F;39-235/Domain: cytokine receptor homology <CRS1>
F;253-434/Domain: cytokine receptor homology <CRS2>
F;442-463/Domain: transmembrane #status predicted <TM>
F;464-896/Domain: intracellular #status predicted <INT>

Query Match 8.3%; Score 173.5; DB 1; Length 896;

Best Local Similarity 20.7%; Pred. No. 7.3e-06;
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

QY 5 CLATGCLYTFLLISTTFTGCTSSDTEIK-----VNPQDFEIVDPGVLGYL 48
DB 94 CVPRRCVLPY---TRFSITNEDYYSFRPDSGLQIOLMVPLAQNVOPPLPKNVSISSSEDR 150
QY 49 LYLOQWQPLP---SLDHFKECTVEYELKYNIGSETWKTITKLNHYKDGFDLNGK 100
DB 151 FLEWVSLSLGDQAQVSWLSKRDIEFEVAYKRL-QDSWEDAYSLSHTSKFQVNFEPKFLPNS 209
QY 101 IEA-KIHT-LLPWOCTNGSEVQSSWAETTYWISPGIPETKQVDMDCVYNNWVLLCSWK 158
DB 210 IYAPRVTRTRYPGSSLSGR--PSRWSPEAHWDSQPG-DKAQPNQLQCFDGIQSLHCSWE 266
QY 159 PGIGVLLDTNLYNFWYEGLDHALQVDYIK-ADGQNI---GCRFPYLEASDYKDFYIC 213
DB 267 VWTOTTSVSGFLFYRSPVAPEEKSPVVKPEPPGASVYTRYHCSLSPVPEPSAHSQYTVS 326
QY 214 VNGSENKPIRSSYFTFOLQNIIVKPLPVPVLTFTRESSCEIKLKWISPLGPIPARCFDYE 273
DB 327 V-----KHLEQGFIMSYNHIOQEPPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ 377
QY 274 IEIREDDTLVTATVEN--EYTLTKTNETRQICFVVRKSVNIYCSDDGIWSEWSKQCV 331
DB 378 VQYKKKSDSWEDSKTENLDRAHSMDLSOLEPDTSYCARVRVVKPISNYDGIWSEWSKSEVTV 437
QY 332 EGEDLSKTKLLRFLWLPFGFILVIVFTVGLL 363
DB 438 K-TDWVMPPL---WI-----VLILVFLILTLFL 461

RESULT 13
I45971
prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C;Accession: I45971
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A;Reference number: I45971; MUID:93246019
A;Accession: I45971
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-581 <SCO>
A;Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C;Genetics:
A;Gene: PRLR
C;Superfamily: cytokine receptor homology
F;36-221/Domain: cytokine receptor homology <CRS>

Query Match 8.0%; Score 167; DB 2; Length 581;
Best Local Similarity 28.5%; Pred. No. 1.4e-05;
Matches 72; Conservative 36; Mismatches 121; Indels 24; Gaps 11;

QY 136 PETKQVDMDCVYNNWVLLCSWKPGIGVLLDTNLYNFWYEGLDHALQVDYIKADGQNI 195
DB 27 PPEKPLVKRSPGKGTFTCWEEFGADGLPTNTLYTHKEGETLIHECPDY-KTGGPN- 84
QY 196 GCRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIIVKPLPVPVLTFTRESSCEIK 255
DB 85 SCYFSKHTSIWKMYVITVAINQMGISSSDPLVHVHYIIVEPPANLLEUKHPEDRK 144
QY 256 ----LKWSIP-LGPIPARCF--DYEIEIREDDTLVTATVENET-YTLKTTN-ETROLCF 306
DB 145 PYLWIKWSPPTMDVKSGWFIQYIEIRLKPEKAT-----DWETHFTLKQTLKIFNLYP 198
QY 307 VVRKSVNIYCS-DDGIWSEWSKQCV--GEDLSKTKLLRFLWLPFGFILVIVFTVGLL 363
DB 199 GQYLVQIRCKPDHGYWSEWSPESSIQIPNDFPVKDTSMWIFVAILSAVICLIWVAVAL 258

A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000
C:Accession: A41070; I55417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin receptor
A:Reference number: A41070; MUID:92041B34
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 [XALI>](#)
A:Cross-references: GB:M74152; NID:3206389; PIDN:AAA41946.1; PID:3206390
R:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
A:Reference number: I55417; MUID:95014432
A:Accession: I55417
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-412 [<RES>](#)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:17:44 ; Search time 13.12 Seconds
(without alignments)
986.934 Million cell updates/sec

Title: US-09-077-817-12

Perfect score: 2087

Sequence: 1 MAFVCLATGCLYFLISTTF.....TGLLRKNTYPMVRCVTL 378

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|-------------|
| 1 | 2059 | 98.7 | 380 | 1 | IL132_HUMAN |
| 2 | 309.5 | 14.8 | 420 | 1 | IL5R_HUMAN |
| 3 | 294.5 | 14.1 | 424 | 1 | IL31_MOUSE |
| 4 | 294.5 | 14.1 | 427 | 1 | IL131_HUMAN |
| 5 | 261 | 12.5 | 831 | 1 | PRLR_CHICK |
| 6 | 241 | 11.5 | 415 | 1 | IL5R_MOUSE |
| 7 | 238 | 11.4 | 831 | 1 | PRLR_MELGA |
| 8 | 220 | 10.5 | 369 | 1 | PRLR_HUMAN |
| 9 | 216.5 | 10.4 | 830 | 1 | PRLR_COLLI |
| 10 | 212.5 | 10.2 | 369 | 1 | CYRG_MOUSE |
| 11 | 208 | 10.0 | 373 | 1 | CYRG_CANFA |
| 12 | 195 | 9.3 | 878 | 1 | IL3B_MOUSE |
| 13 | 189.5 | 9.1 | 379 | 1 | CYRG_BOVIN |
| 14 | 178.5 | 8.6 | 897 | 1 | CYRE_HUMAN |
| 15 | 173.5 | 8.3 | 896 | 1 | CYRB_MOUSE |
| 16 | 167 | 8.0 | 581 | 1 | PRLR_BOVIN |
| 17 | 166 | 8.0 | 610 | 1 | PRLR_RAT |
| 18 | 159 | 7.6 | 608 | 1 | PRLR_MOUSE |
| 19 | 153 | 7.3 | 616 | 1 | PRLR_RABIT |
| 20 | 151 | 7.2 | 622 | 1 | PRLR_HUMAN |
| 21 | 151 | 7.2 | 862 | 1 | IL2S_HUMAN |
| 22 | 150.5 | 7.2 | 917 | 1 | IL6B_MOUSE |
| 23 | 150 | 7.2 | 581 | 1 | PRLR_CEREL |
| 24 | 142.5 | 6.8 | 400 | 1 | GMCR_HUMAN |
| 25 | 138 | 6.6 | 378 | 1 | IL3R_HUMAN |
| 26 | 134.5 | 6.4 | 1097 | 1 | LIFR_HUMAN |
| 27 | 131.5 | 6.3 | 630 | 1 | PRLR_ORENI |
| 28 | 128 | 6.1 | 874 | 1 | IL2S_MOUSE |
| 29 | 126.5 | 6.1 | 918 | 1 | IL6B_HUMAN |
| 30 | 120.5 | 5.8 | 836 | 1 | GCSR_HUMAN |
| 31 | 113.5 | 5.4 | 1165 | 1 | LEPR_HUMAN |
| 32 | 112.5 | 5.4 | 1630 | 1 | PTPL_DROME |
| 33 | 109.5 | 5.2 | 918 | 1 | IL6B_RAT |

34 107.5 5.2 638 1 GHR_HUMAN
35 107.5 5.2 837 1 GCSR_MOUSE
36 107 5.1 634 1 GHR_BOVIN
37 106 5.1 634 1 GHR_SHEEP
38 105 5.0 511 1 VGLG_VSVO
39 104.5 5.0 1092 1 LIFR_MOUSE
40 102.5 4.9 638 1 GHR_PIG
41 101.5 4.9 638 1 GHR_RABIT
42 99.5 4.8 1162 1 LEPR_RAT
43 99 4.7 638 1 GHR_RAT
44 98.5 4.7 1162 1 LEPR_MOUSE
45 98 4.7 511 1 VGLG_VSVIG

ALIGNMENTS

RESULT 1
IL132_HUMAN
ID IL132_HUMAN STANDARD; PRT; 380 AA.
AC Q14627; O00667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13
DE BINDING PROTEIN).
GN IL13RA2 OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=96279273; PubMed=86631118;
RA Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N.,
RA Ferrara P.;
RT "Cloning and characterization of a specific interleukin (IL)-13
RT binding protein structurally related to the IL-5 receptor alpha
RT chain.";
RL J. Biol. Chem. 271:16921-16926(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97321053; PubMed=9177784;
RA Guo J., Apio F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;
RT "Chromosome mapping and expression of the human interleukin-13
RT receptor.";
RL Genomics 42:141-145(1997).
CC -I- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13
CC (IL-13), BUT NOT TO IL-4.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL; X95302; CAA64617.1; -;
DR EMBL; U70981; AAB17170.1; -;
DR EMBL; Y08768; CAA70021.1; -;
DR MIM; 300130; -;

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DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3.1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;

Query Match 98.7%; Score 2059; DB 1; Length 380;
Best Local Similarity 99.7%; Pred. No. 4.4e-161;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQDPFEIYDVGILYGLYQWOPPLSLD 60
Db 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQDPFEIYDVGILYGLYQWOPPLSLD 60
Qy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKHTLLPQCCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKHTLLPQCCTNGSEVQ 120
Qy 121 SSWAETTWISQGPETKVDQDCVYVWYLLCSWKPGLVLDITVATVETNYTLTKTNE 180
Db 121 SSWAETTWISQGPETKVDQDCVYVWYLLCSWKPGLVLDITVATVETNYTLTKTNE 180
Qy 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFICVNGSENKPIRSSYFTFQQLNIVKPLP 240
Db 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFICVNGSENKPIRSSYFTFQQLNIVKPLP 240
Qy 241 PVYLFTRESSECEIKLWSIPLGPAPCFDYEIEIREDDITLVATVETNYTLTKTNE 300
Db 241 PVYLFTRESSECEIKLWSIPLGPAPCFDYEIEIREDDITLVATVETNYTLTKTNE 300
Qy 301 TRLQCFVYRSVKNVYCSDDGIWSEMSDKQCEGEDLSKTLRLFWLPGFILLIVIFVTG 360
Db 301 TRLQCFVYRSVKNVYCSDDGIWSEMSDKQCEGEDLSKTLRLFWLPGFILLIVIFVTG 360
Qy 361 LLLRKPNTYPRMW 373
Db 361 LLLRKPNTYPRMI 373

RESULT 2
IL5R_HUMAN
ID IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125
DE ANTIGEN).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
[2]

SEQUENCE FROM N.A.
RP MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of
RT the human interleukin 5 receptor alpha subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
[3]
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT an IL5-specific alpha chain and a beta chain shared with the receptor
RT for GM-CSF";
RL Cell 66:1175-1184(1991).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide Cdw125 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
-----
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DR EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A26249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A26251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; 147851; -.
DR InterPro; IPR000950; -.
DR InterPro; IPR002465; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420
FT DOMAIN 21 342
FT TRANSMEM 343 362
FT DOMAIN 363 420
FT CARBOHYD 35 35
FT CARBOHYD 131 131
FT CARBOHYD 216 216
FT CARBOHYD 244 244
FT VARSPLIC 333 335
FT VARSPLIC 336 420
FT VARSPLIC 334 333
FT VARSPLIC 334 420
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NDE -> FSR (IN SOLUBLE ISOFORM S1).
MISSING (IN SOLUBLE ISOFORM S1).
N -> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
Query Match 14.8%; Score 309.5; DB 1; Length 420;
Best Local Similarity 27.6%; Pred. No. 4.4e-18;
Matches 98; Conservative 65; Mismatches 151; Indels 41; Gaps 15;

Qy 27 DTEIKVNPQDPFEIYDVGILYGLYQWOPPLSLDFHFEKTYEYELKYRNIGSETWKTIT 86
Db 25 DEKISLLPPVNFITKVIG-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPDEDTYETRIT 82
```


QY 87 KNLHYKGDGLNKGIEAKIHTLLPQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
 DB 83 ES---KCVTILHKGSASVRLTQ---NDHSLSSWASAEHL-APPGSPGTSIVNLCT 135
 QY 147 -----YNNQYLL-CSWKPGIGVLLDTNNLYF-----WEGDLHALQVDYIKAD 191
 DB 136 TMTEDNTSRUSRYQVSLHCTVLGTDAPEQTQVFLYRYGSWTE-----ECQEYSKDT 189
 QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSEKPIRSSYFTFQLOKIVKPLPPVYLTFT 248
 DB 190 LGRNIACWFPRTFILSKGRDWSLVYNGSSKHSARPDQFLFALHAIQINPLNVTAEI 249
 QY 249 ESSCEIKLWSIPLGIPARCFDYEIREDDTLTIVATVENETYLTKTNETRQLCFV 308
 DB 250 EGT-RLSIQWEKPVSAFFHCFDYEVKTHNTRNGVYLQIEKLTNAFISIIDLSKYDVQV 308
 QY 309 RSKVNIYSDGINSWEDSKQCEGDSKTLRFLWLPFGFILLILVFTVGLLL 363
 DB 309 RAASVSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILL 356

RESULT 3
 IL131_MOUSE
 ID IL131_MOUSE STANDARD; PRT; 424 AA.
 AC O09030;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).
 GN IL13RA1 OR IL13RA OR IL13R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96133964; PubMed=8552669;
 RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A., Willson T.A.;
 RA "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
 CC -!- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).
 CC -!- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC -----
 DR MGD; S80963; AAB50695.1; -;
 DR MGD; MGI:105052; IL13ra.
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 424 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
 FT DOMAIN 26 340 EXTRACELLULAR (POTENTIAL).

TRANSMEM 341 364 POTENTIAL.
 DOMAIN 365 424 CYTOPLASMIC (POTENTIAL).
 FT 37 100 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 44 93 POTENTIAL.
 FT DISULFID 132 142 BY SIMILARITY.
 FT DISULFID 171 183 BY SIMILARITY.
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 424 AA; 4840 MW; EB8330A0DC82CF9 CRC64;

Query Match 14.18; Score 294.5; DB 1; Length 424;
 Best Local Similarity 25.88; Pred. No. 7.5e-17;
 Matches 102; Conservative 68; Mismatches 151; Indels 75; Gaps 19;

QY 8 IGCLYTFELIST-TFCCTSSSDTEIKVNPQQDFEIVDPGCLGYLQWOPPLSLDHFKECT 66
 DB 7 LGELLVLLWTATVGOVAAA---TEVQPPVTNLSVSVENLCTIITWSPPEGAS--PNCT 61
 QY 67 VEY-----ELKRYNIGSTWTKIITKNLHYKGDGLNKGIEAKIHTLLPQCT-NGSEVQ 120
 DB 62 LRYFSHFDDQDKKIAPET-----HREELPLDEKICLQVGS---QCSANESEKP 108
 QY 121 SSWAETTYWIS-POGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNNLYFWYEGDL 179
 DB 109 SPLVKKC--ISPPGDPESAVTEKLCIWHNLSYKCSLWLPGRNTSPDTHYLYYISLE 166
 QY 180 HALQVDYIKADQGNIGCRFPYLEAS---DYKDFYICVNGSSSEKPIRSSYFTFQLOKIV 236
 DB 167 KSROC-ENIYREGQHIACSFKLTKVEPSFEHQNVQIMVKDNAGK--IRPSKIVLSISYV 223
 QY 237 KPLPPVYLTFTRESCEIKLWSIPLGIPARCFDYEIEIR----- 277
 DB 224 KPDPH-HIKHLLKNGALLVQWKNPN--FRSRCLTYEVEVNTQTDHRNILEVEEDKQCN 281
 QY 278 -EDDTTL-----VTATVENETYLTKTNETRQLCFVVRVSKVNIYSDGINSWEDSKQ 329
 DB 282 SESRNMEGTSCFGLPGVLADAVYTVRVKTNKLCF-----DDNKLNSDWSEAQ 331
 QY 330 CWEGEDLSK-KTLRFLWLPFGFILLILVFTVGLLLR 364
 DB 332 SIGKEQNSTFTTMTLLTIPV-FVAVAVILLFLYLR 366

RESULT 4
 IL131_HUMAN
 ID IL131_HUMAN STANDARD; PRT; 427 AA.
 AC P78552; O99656; O95646;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1).
 GN IL13RA1 OR IL13RA OR IL13R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Carcinoma;
 RX MEDLINE=97165986; PubMed=9013879;
 RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N., Ferrara P.;
 RA "Cloning of the human IL-13R alpha1 chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex.";
 RL FEBS Lett. 401:163-166(1997).
 RN [2]
 RP SEQUENCE FROM N.A.


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DR HSP; P16471; IBP3.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSSEM 439 459
FT DOMAIN 460 831
FT DOMAIN 123 225
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT CARBOHYD 75 86
FT CARBOHYD 59 91
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94102 MW; 1C4E7579IDCABE9 CRC64;

Query Match 12.5%; Score 261; DB 1; Length 831;
Best Local Similarity 26.3%; Pred. No. 9.4e-14;
Matches 98; Conservative 55; Mismatches 175; Indels 44; Gaps 16;

QY 18 TTFCTSSSTEIKVN--PQDFE---IVDPG-----YLGYLQWQPLSL 59
DB 97 TTFNITVATNEIGNSSDPQYVDVTISVPGSPVNLTLTKRSANIMYLWAKWSPLLA 156
QY 60 DHFKECTVEYELKRNIGSETWKTIIKNLHYKDGFDLNGKIEAKIHTLLPQCTNGSEV 119
DB 157 DASSNHLHYELRLKPEKEWEI---SVGVQVQCKINR--LNAGMYVVOVRCITLDPGE 212
QY 120 QSSWAETTYWISPOG-IPETKVQDMDCVYVYVWQYLLCSWRKPGIGVLLDTNLFYFWEGL 178
DB 213 WSESSERHILPSQSPPEKPTIIKCRSPEKETFTCKWPKGLDGHPTNLYLSKEGE 272
QY 179 DHALQCVDIKADQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLQNVKP 238
DB 273 EQVYECPDY-RTAGPN-SCYFDKKHTSFWTIYNTVTRATNMGSSNSDPHYVDVYIVQP 330
QY 239 LPPVLTFTRESSCEIK---LKWS-IPLGPAPARCFDYEIR---EDDTLLVTATVEN 290
DB 331 DPNVNTLELKKPINRKPVLVLTWSPPLADVRSGWLTLEYELRLKPEGEWEITFVQ 390
QY 291 ET-YTLKTTNETROLCFVRSKVNIIYSD--GIWSEWSDKQCWE--GEDLSKTKLLRFLW 346
DB 391 QYQYKMFSLNPGKKYI-----IQHCKPDHGHGSEWSENENYIPIENPRVKDMI-VWI 443
QY 347 PFGILLIVFV 358
DB 444 VLGVSLSLICLI 455

RESULT 6
IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).
GN IL5RA OR IL5R.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA Takatsu K.;
RT "Molecular cloning and expression of the murine interleukin-5
receptor.";
RL EMBO J. 9:4367-4374(1990).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC -!- BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC ON B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90205; BAA14231.1; -.
DR PIR; S12357; S12357.
DR MGD; MGI:96558; IL5ra.
DR InterPro; IPR000950; -.
DR InterPro; IPR002465; -.
DR PROSITE; PS01352; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415
FT DOMAIN 18 339
FT TRANSSEM 340 361
FT DOMAIN 362 415
FT DISULFID 131 152
FT DISULFID 179 193
FT CARBOHYD 32 32
FT CARBOHYD 128 128
FT CARBOHYD 213 213
FT CARBOHYD 241 241
SQ SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 11.5%; Score 241; DB 1; Length 415;
Best Local Similarity 24.9%; Pred. No. 1.7e-12;
Matches 80; Conservative 65; Mismatches 144; Indels 56; Gaps 17;

QY 34 PPQDFEIVDPGYLGYLQWQPLSLDHFRECTVEYELKRNIGSETWKTIIKNLHYKD 93
DB 29 PPVNFITKATG-LAQVLLHNDPNPDQEQ-RHVDLEYHVKINAPQEDVDTRKTES---KC 83
QY 94 GFDLNGKIEAKIHTLLPQCTNGSEVSSNAETTYWISPOGIPETKVQDMDCVYV--- 149
DB 84 VTPLHEGFAASVRLTK---SSHTTLASSWVSABL-KAPPGSPGTSVNTLCTTHTVVS 139
QY 150 -----WQY-LLCSWKPGIGVLLDTNLFYFWEGLDHALQCVDIK-ADGONIGCRFP- 200
DB 140 HTHLRPYQVSLRCTLVKGKAPEDTQYLYRFGVLTE--KCQETSRDALNRNTACFP 197
QY 201 -YLEASDKDFYICVNGSSSENKPIRSYFTFQLQNVKPLPPVLTFTRESSCEIKLWS 259
DB 198 TFINSKGEQLAVHINGSKRAALKKPDQLFSLAIDQVNPVNTVEIESN-SLYIOWE 256
QY 260 IPLGPIPARCFDYEIREDD-----TTLVATVENETTYLTKTTNETROLCFV 308
DB 257 KPLSAFPDHCNFYELKIYNTKNGHIQKELIANKFISKIDDVSTYSIQ-----V 305

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CC EMBL; D11086; BAA01857.1; -.
CC EMBL; L12183; AAA59145.1; -.
CC EMBL; L12178; AAA59145.1; JOINED.
CC EMBL; L12176; AAA59145.1; JOINED.
CC EMBL; L12177; AAA59145.1; JOINED.
CC EMBL; L12179; AAA59145.1; JOINED.
CC EMBL; L12180; AAA59145.1; JOINED.
CC EMBL; L12181; AAA59145.1; JOINED.
CC EMBL; L12182; AAA59145.1; JOINED.
CC EMBL; L19546; AAC37524.1; -.
CC PIR; A42565; A42565.
CC PDB; 1ILM; 26-JAN-95.
CC PDB; 1ILN; 26-JAN-95.
CC MIM; 308380; -.
CC MIM; 300400; -.
CC InterPro; IPR000950; -.
CC InterPro; IPR001777; -.
CC InterPro; IPR002465; -.

Query Match      10.5%; Score 220; DB 1; Length 369;
Best Local Similarity 25.5%; Pred. No. 7.8e-11;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

Qy 97 LNKGEAKIHITLLPQCTNGSE-VQSSWAETTYWISQIGIPETKVQDMDCVYVWQYLLC 155
Dy 19 LGVGLNTTILT-----PNGNEDTADFFLTMTPTDSLSVSTPLPEVQCFVNFVYVNC 72

Qy 156 SW-----KPGIGVLDITNLYVYEGLDH--ALQCVDIKADQNGICRFPYLEASDY 207
Dy 73 TWNSSESPQP-----TNLTLYWKNSDNDKVKCKSHLYFSEITSGCQLOKKEIHL 125

Qy 208 KDFYICVNGSSSENPIRSSYFTFQNLQIVKPLPPVYLFTFTRESSCEIKLKWISPLGPEPA 267
Dy 126 QTFVQLQDPRE--PRQATQMLQNLVLPWAPENLTLLKLSQLELNNW---NRFLN 180

Qy 268 RCFDYETEIRSD-DTTLVTATVE-NERYTLKTNETQLCFVRSKVNICYSDDGISEW 325
Dy 181 HCLEHLVQYRTDWDHSTEQSVYRHKFSVPSVQGRKRYTFRVRSRPNLPGSAQHSEW 240

Qy 326 SDKQCEGEDSKKTLRFLWLPFGFILILVIFVVG 360
Dy 241 SHPIHW-GSNTSKEN-----PFLFAEAVVISVG 268

RESULT 9
PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374; PRLR_COLLI STANDARD; PRT; 830 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor."
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

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CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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EMBL; U07694; AAA20646.1; -.
HSSP; P16471; IBP3.
InterPro; IPR000950; -.
InterPro; IPR001777; -.
InterPro; IPR002465; -.
Pfam; PF00041; fn3; 4.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT CARBOHYD 316 316
FT CARBOHYD 336 336
FT SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFF CRC64;

Query Match      10.4%; Score 216.5; DB 1; Length 830;
Best Local Similarity 24.4%; Pred. No. 4e-10;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

Qy 18 TTFCTSSSTDEIKVNPQDFEIVDPQYLG-----DPQYVDVTISVQPDAPVNLSTETKSASTTYLLAKW 150
Dy 97 TTYNTITVAMNEIGSNSS-----DPQYVDVTISVQPDAPVNLSTETKSASTTYLLAKW 150

Qy 54 QPPLSLDHFKECTV-EYELKYRNIGSETWKTITKNLHYKDGFLNKGIEAKIHTLLPWQ 112
Dy 151 SPPLADVTNSHVRYELRLKPEKEWEIV---SVGVQYQVKNR-LQAGVYVQVR 206

Qy 113 CTNGSEVQSSWAETTYWISQIG-IPETKVQDMDCVYVWQYLLCSWRPGIGVLDITNVL 171
Dy 207 CVLDIGSEWSSSRHIHPNGESPPKEPTIIKCRSPEKETFTCWKPKSGDGGHTNYTL 266

Qy 172 FYWVEGLDHALQVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENPIRSSYTFQ 231
Dy 267 LYSKEGEERYVECPDY-KTAGPN-SCYFDKKHTSWFTYINITVKATNEIGSNVDPLVD 324

Qy 232 LQNIKVLPPVYLTFTRESSCEIK-----LKWS-IPLGPIPA--RCFDYETEIRSDDTTLV 284
Dy 325 VTYIVQDPPVNVTLKTKVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKEEA--- 381

Qy 285 TATVENEYTLTKTNETRQLCFVY-----RSKNVICYSD--GIWSEWS-DKQCEGEDLS 337
Dy 382 -----EEWETIFVQOQTHYKMFSLNPKCKYIVQIHCKPDHHSWSEWSLEKYLQIPTDFR 436

Qy 338 KTLRLRFLWLPFGFILILVIFV 358
Dy 437 IKDMV-VMIIVGVLSLCLV 456


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RESULT 10
CYRG_MOUSE
ID CYRG_MOUSE STANDARD; PRT; 369 AA.
AC P34902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors."
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CBA/CA;
RA Cao X., Kozak C.A., Liu Y.J., Nequchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RT Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma."
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT chromosomal localization and expression in the adult thymus."
RL Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=B6.S;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44."
RL J. Neurocol. 26:231-239(1995).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
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DR EMBL; D13821; BAA02974.1; -

DR EMBL; U21795; AAA64279.1; -

DR EMBL; D13565; BAA02760.1; -

DR EMBL; L20048; AAA39286.1; -

DR EMBL; S75852; AAB32904.1; -

DR EMBL; S75844; AAB32904.1; JOINED.

DR EMBL; S75845; AAB32904.1; JOINED.

DR EMBL; S75847; AAB32904.1; JOINED.

DR EMBL; S75848; AAB32904.1; JOINED.

DR EMBL; S75849; AAB32904.1; JOINED.

DR EMBL; S75850; AAB32904.1; JOINED.

DR EMBL; S75851; AAB32904.1; JOINED.

DR EMBL; X75337; CAA53085.1; -

DR PIR; JN0592; JN0592.

DR PIR; JN0775; JN0775.

DR HSSP; P31785; ILIN.

DR MGD; MGI:96551; IL2rg.

DR InterPro; IPR000950; -

DR InterPro; IPR001777; -

DR InterPro; IPR002465; -

DR Pfam; PF00041; fn3; 1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.

FT DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 264 284 POTENTIAL.

FT DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 151 250 FIBRONECTIN TYPE-III.

FT DISULFID 62 72 POTENTIAL.

FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 369 AA; 42241 MW; CB2D5AB459077AC7 CRC64;

Query Match 10.28; Score 212.5; DB 1; Length 369;

Best Local Similarity 26.9%; Pred. No. 3.2e-10;

Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKVDMDCVYVNOYLCSW----KPGIGVLLDTNVLNLFYVYEGLDHAL--OCVDYIK 189

Db 53 PTLPLPEVQCVFVNIEMNCTWNSSEPQA-----TNLTLYRKVSDNNTFQBCSHYLF 107

QY 190 ADGNIGCRFPYLEADYKDFYICVNGSSSENKPIRSYFTFQIQNIYKPLPPVYLTFTRE 249

Db 108 SKETISGCIQKEDIQLYQYFVVQL--QDPKQPORRAVQKLNQLNVLPRAPENLTLSNL 165

QY 250 SSEIKLKWSIPGIPARCFDYIEIREDDTLVATVENE--TYTLKTTNETRQLCFV 307

Db 166 SESOLELRWK--SRHIKERCLQVLYOYRNRDRSWTEILVNHPEFSLPSYDELKRYTFR 223

QY 308 VRKRVNIYSDDDGIWSEMSDKQWEG---EDLSKTKLLRFLWLPFGF--ILILVIFVTGL 361

Db 224 VRKRVNIYSDDDGIWSEMSDKQWEG---EDLSKTKLLRFLWLPFGF--ILILVIFVTGL 361

QY 362 LLRRKPTNPY 370

Db 284 LERMPPIPP 292

RESULT 11

ID CYRG_CANFA STANDARD; PRT; 373 AA.

AC P40321;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)

Query Match 9.3%; Score 195; DB 1; Length 878;
 Best Local Similarity 24.1%; Pred. No. 2.5e-08;
 Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

QY 34 PPQDFEIVDPGLYGLVLOWQPLP---SLDFKBCCTVEYELKYNIGSETWKTITNLH 90
 Db 139 PKDHIHSPSG---DHFLEWSVSLGDSQVSWLSKIDFEFVAYKRL-ODSWED--ASSLH 193
 QY 91 YKDGFDLKNKGIEAKIHTLLP-----WQCTNGSEVQ-----SSWAETTYWISPGQIPET 138
 Db 194 -TSNFQVN--LEPKL--FLPNSIYAARVRLSAGSSLSGRPSRWSPEVHWSQF-DKA 247
 QY 139 KVQDMCVYVNWQYLLSGPGIGVLDNTNLYFYWEGLDHALQCVDYIKADQONI--- 195
 Db 248 QPQNLQCFDFDQISLHCSWEVMTQTGVSFGLFYRSPAAPEEKSPVVKPQASVYTR 307
 QY 196 -GCRFPYLEADYKDFYICVNGSSNKPPIRSYFTFQNLQVKNLPLPVY-LTFTRESSCE 253
 Db 308 YRCSLPVPEPSAHSQYTVSVKHLQGGKFI-MSYHYIQME-----PILNQTKNRDS--- 357
 QY 254 IKLKWISPLGPIPARCFD--YEIEIREDDTLVTATVEN-----ETYTLKTTNETRQLCFV 307
 Db 358 YSLHWETQKIP---KYDHTFQVQYKKKSKESKDKSTENLGRVNSMDLPQLEPDTSYCAR 414
 QY 308 VRSK-VNIYCSDDGINSWSDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTGLL 363
 Db 415 VRVKPISDY---DGINSEWSNEYTWT-TDWMPYL---WI---VLIIVFLIFLITLL 460

RESULT 13
 CYRG_BOVIN STANDARD; PRT; 379 AA.
 AC Q95118;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
 DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
 GN IL2RG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96268473; PubMed=8672241;
 RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
 RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
 gamma gene";
 RL DNA Cell Biol. 15:453-459(1996).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 CC EMBL; U33748; AAB07812.1; -
 CC HSPSP; P31785; IILN.
 CC InterPro; IPR000950; -
 CC InterPro; IPR001777; -
 CC InterPro; IPR002465; -

Pfam; PF00041; fn3; 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
 FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 270 290 POTENTIAL.
 FT DOMAIN 291 379 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 158 256 FIBRONECTIN TYPE-III.
 FT DISULFID 68 78 POTENTIAL.
 FT DISULFID 109 122 POTENTIAL.
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.1%; Score 189.5; DB 1; Length 379;
 Best Local Similarity 26.2%; Pred. No. 2.5e-08;
 Matches 62; Conservative 42; Mismatches 106; Indels 27; Gaps 9;

QY 135 IPEKTVQDMCVYVNWQYLLCSW-----KPGIGVLDNTNLYFYWY---EGLDHALQCV 185
 Db 61 LPLPKVQ---CFVFNVEYMNCTWNSSEPQP-----NNLTLYGYRNFNGDDKLQECG 110
 QY 186 DYIKADQNTGCRFPYLEADYKDFYICVNGSSNKPPIRSYFTFQNLQVKNLPLPVYLT 245
 Db 111 HYLFGEGITGCGWFGKKEIRLYETFFVOLQDPREHR--KOPKQMKLQDLVWPAPENLT 168
 QY 246 FTRESSCEIKLKWISPLGPIPARCFDYEIEIREDDTLVTATVEN-ETYTLKTTNETRQ 303
 Db 169 LRNLSEFQLELSWS---NRYLDHCLHLVQYRSRDRSWSFQSVDRHSFSLPSVDAQKL 225
 QY 304 LCFVVRKVNIIYCSDDGINSWSDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 Db 226 YTFVRVSRYNPLCGSQAHSWSDSYPIHW-GSNTSKENIENPENPSLFALEAVLIPLG 281

RESULT 14
 CYRG_HUMAN STANDARD; PRT; 897 AA.
 AC P32927;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR (CDW131 ANTIGEN).
 GN CSF2RB OR IL5RB OR IL3RB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91088571; PubMed=1702217;
 RA Havashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
 RA Miyajima A.;
 RT "Molecular cloning of a second subunit of the receptor for human
 RT granulocyte-macrophage colony-stimulating factor (GM-CSF):
 RT reconstitution of a high-affinity GM-CSF receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
 RN [2]
 RP REVISION TO 454.
 RA Kitamura T.;
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
 CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:17:29 ; Search time 24.61 seconds
(without alignments)
2032.154 Million cell updates/sec

Title: US-09-077-817-12

Perfect score: 2087

Sequence: 1 MAFVCLAIGCLYELISTTF.....TGLLLRKNTYPKMVRCTL 378

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protein:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1194.5 | 57.2 | 383 | 11 | O88786 |
| 2 | 310.5 | 14.9 | 420 | 4 | Q14633 |
| 3 | 309.5 | 14.8 | 396 | 4 | Q14631 |
| 4 | 292 | 14.0 | 333 | 4 | Q15469 |
| 5 | 291.5 | 14.0 | 415 | 11 | Q920K4 |
| 6 | 264.5 | 12.7 | 349 | 6 | O97597 |
| 7 | 241.5 | 11.6 | 279 | 4 | Q9UDY5 |
| 8 | 197.5 | 9.5 | 363 | 13 | Q9DEQ1 |
| 9 | 185.5 | 8.9 | 611 | 13 | Q9PTI0 |
| 10 | 185.5 | 8.9 | 611 | 13 | Q9IBF6 |
| 11 | 178 | 8.5 | 896 | 11 | Q64146 |
| 12 | 173.5 | 8.3 | 881 | 13 | O57519 |
| 13 | 172 | 8.2 | 611 | 13 | O9PTH9 |
| 14 | 170 | 8.1 | 890 | 11 | Q921A0 |
| 15 | 169 | 8.1 | 227 | 6 | Q9GLW3 |
| 16 | 167 | 8.0 | 296 | 6 | O18880 |
| 17 | 167 | 8.0 | 622 | 6 | Q9N0J7 |
| 18 | 161 | 7.7 | 581 | 6 | O46561 |
| 19 | 156 | 7.5 | 625 | 6 | Q9XS92 |

| | | | | | |
|----|-------|-----|------|----|--------|
| 20 | 153.5 | 7.4 | 918 | 13 | Q9W6U9 |
| 21 | 153 | 7.3 | 217 | 6 | O46386 |
| 22 | 151 | 7.2 | 206 | 4 | O16354 |
| 23 | 151 | 7.2 | 349 | 4 | Q9UHJ5 |
| 24 | 147.5 | 7.1 | 538 | 13 | Q9DFU0 |
| 25 | 146.5 | 7.0 | 422 | 4 | Q9UHH5 |
| 26 | 145.5 | 7.0 | 422 | 4 | O75462 |
| 27 | 143.5 | 6.9 | 425 | 11 | Q9JM58 |
| 28 | 138 | 6.6 | 390 | 4 | Q9UEH7 |
| 29 | 135 | 6.5 | 346 | 13 | O93404 |
| 30 | 130.5 | 6.3 | 198 | 6 | O18985 |
| 31 | 126.5 | 6.1 | 329 | 4 | Q9UQ41 |
| 32 | 119.5 | 5.7 | 371 | 4 | Q9HC73 |
| 33 | 117.5 | 5.6 | 896 | 4 | O13594 |
| 34 | 117.5 | 5.6 | 906 | 4 | O13593 |
| 35 | 117.5 | 5.6 | 958 | 4 | O13592 |
| 36 | 116.5 | 5.6 | 1282 | 5 | Q9VWE0 |
| 37 | 114 | 5.5 | 894 | 6 | Q9MYL1 |
| 38 | 114 | 5.5 | 925 | 6 | Q9MYK9 |
| 39 | 114 | 5.5 | 1163 | 6 | Q9MYL2 |
| 40 | 114 | 5.5 | 1194 | 6 | Q9MYL0 |
| 41 | 113.5 | 5.4 | 896 | 4 | O92919 |
| 42 | 113.5 | 5.4 | 958 | 4 | O92920 |
| 43 | 113.5 | 5.4 | 1165 | 4 | O92921 |
| 44 | 111 | 5.3 | 628 | 11 | Q9JKG1 |
| 45 | 110 | 5.3 | 6875 | 6 | Q28733 |

ALIGNMENTS

| | | | | | |
|--------|--|--------------|------|-----|-----|
| RESULT | 1 | | | | |
| O88786 | | | | | |
| ID | O88786 | PRELIMINARY; | PRT; | 383 | AA. |
| AC | O88786; | | | | |
| DT | 01-NOV-1998 (TREMBLrel. 08, Created) | | | | |
| DT | 01-NOV-1998 (TREMBLrel. 08, Last sequence update) | | | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | | | | |
| DE | IL-13 RECEPTOR ALPHA 2. | | | | |
| GN | IL13RA2. | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C3H/HEJ; TISSUE=THYMUS; | | | | |
| RX | MEDLINE=98391042; PubMed=9725226; | | | | |
| RA | Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H., | | | | |
| RA | Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R., | | | | |
| RA | Collins M.; | | | | |
| RT | "The murine IL-13 receptor alpha 2: molecular cloning, | | | | |
| RT | characterization, and comparison with murine IL-13 receptor alpha 1."; | | | | |
| RL | J. Immunol. 161:2317-2324(1998). | | | | |
| DR | EMBL; U65747; AAC33240.1; - | | | | |
| DR | MED: 1277954; IL13ra2. | | | | |
| DR | InterPro; IPR002996; - | | | | |
| DR | InterPro; IPR003532; - | | | | |
| DR | PROSITE; PS01356; HEMATOPO_REC_SF2; UNKNOWN.1. | | | | |
| SQ | SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64; | | | | |

| | | | | |
|-----------------------|------------------|---|-----------|-------------|
| Query Match | 57.2%; | Score 1194.5; | DB 11; | Length 383; |
| Best Local Similarity | 58.9%; | Pred. No. 1.3e-98; | | |
| Matches 219; | Conservative 55; | Mismatches 91; | Indels 7; | Gaps 3; |
| QY | 1 | MAFVCLAIGCLYELISTTFGTGSSSTDEIKVNPQDFEIVDPGVLGYLQWPPPLSLD | 60 | |
| Db | 1 | MAFV-HIRCLCILLCTITGYS-----LEIKVNPQDFEILDPLGLLYLQWPPVIE | 54 | |
| QY | 61 | HFRECTVEYELKYNIGSETWTKIITKNLHYKDGFDLNGKIEAKIHTLLFPWCTNGSEVQ | 120 | |
| Db | 55 | KFGCTLEYELKYNVDSDSKTIITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ | 114 | |

| | | | |
|-----------------------|---|--|--------------------------------|
| QY | 121 | SSNAETTYWISPOGIPETKVDQMDCVYNNQYLLCSWKPGIGVLLDTNNLYFWVEGLDH | 180 |
| Db | 115 | SPWIEASYGISDGSLETKIQDKMKCIYVNNQYLVCSWKPGKTVYSTNTYTMFEFWEGLDH | 174 |
| QY | 181 | ALQCVDYIKADGONICGRFPYLEASDYKOFYICVNGSSSENKPIRSSYFTFQLONIKPLP | 240 |
| Db | 175 | ALQCADYLQHDENGVGCKLSNLSYKDFICVNGSSLEPIRSSYFTFQLONIKPLP | 234 |
| QY | 241 | PVYLTFRESCEIKLWSIPLGPIDPARCFDYETREDDTTLVTATVENETVTLKTTNE | 300 |
| Db | 235 | PEFLHISVENSIDIRMKWSPGPIPRCYTYIVIVREDDISWESATDKNDMKLKRANE | 294 |
| QY | 301 | TROLCFVVRKVNICYSDDGISWSDKQCWEGEDLSKKTILARFWLPGFILLILYIVFTG | 360 |
| Db | 295 | SEDLCCFVVRKVNICYADDDGISEWSEECWEGYTPGDSKII-FIVPVCLEFFILLILLIC | 353 |
| QY | 361 | LLLRKPNYPKM | 372 |
| Db | 354 | LIVEKEPEPTL | 365 |
| RESULT | 2 | | |
| Q14633 | | PRELIMINARY; | PRT; 420 AA. |
| ID | Q14633 | | |
| AC | Q14633; | | |
| DT | 01-NOV-1996 (Tremblrel. 01, Created) | | |
| DT | 01-NOV-1996 (Tremblrel. 01, Last sequence update) | | |
| DT | 01-MAR-2001 (Tremblrel. 16, Last annotation update) | | |
| DE | INTERLEUKIN-5 RECEPTOR PRECURSOR. | | |
| DE | HSILSR. | | |
| GN | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| ON | NCBI_TaxID=9606; | | |
| OX | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=PERIPHERAL BLOOD; | | |
| RX | MEDLINE=92121815; PubMed=1732409; | | |
| RT | Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.; | | |
| RT | "Molecular cloning and expression of the human interleukin 5 | | |
| RL | receptor."; | | |
| RL | J. Exp. Med. 175:341-351(1992). | | |
| DR | EMBL; X61176; CAA3483.1; -. | | |
| DR | InterPro; IPR002996; -. | | |
| DR | InterPro; IPR003532; -. | | |
| DR | PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1. | | |
| KW | Signal. | | |
| FT | SIGNAL | 1 20 | POTENTIAL. |
| FT | CHAIN | 21 420 | INTERLEUKIN-5 RECEPTOR. |
| SQ | SEQUENCE | 420 AA; 47670 MW; 8DC56DFC8BEFF524 | CRC64; |
| Query Match | | 14.9%; | Score 310.5; DB 4; Length 420; |
| Best Local Similarity | | 27.9%; | Pred. No. 1.2e-19; |
| Matches | 99; Conservative | 64; Mismatches | 151; Indels 41; Gaps |
| QY | 27 | DTEIKVNPPODFEIVDPGYLGYYLQWPPSLSDHFKECTVEYELKYRNISETWKTIT | 86 |
| Db | 25 | DEKISLLPNNFTIKVTG-LAQVLLQWKNPDQEQ-RNVNLQYQVKINAKEDDVETRI | 82 |
| QY | 87 | KNLHYKDGFLNKGIAKIHILLPWQCTNGSEVQSSWAETTYWISPOGIPEKVVQMDCV | 146 |
| Db | 83 | ES---KCVTLIHKGFSASVTHIQ----NDHSLIASWSASAEIH-APGSPGTSVNLNCT | 135 |
| QY | 147 | -----YYNQYILL-CSWKPGIGVLLDTNNLYF-----WYEGLDHALQCVDYIKAD | 191 |
| Db | 136 | TNTEDNYSRLRSYQVSLHCTVLVGTDAPDQYFLYYRGSKTE-----ECQEYSKDT | 189 |
| QY | 192 | -GNIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIKPLP | 248 |
| Db | 190 | LGRNIAICWFTPTILSKGRDWLAVLVNGSSKSHAIFFPDLQALHAIDQINPLNVTAEI | 249 |

| | | | | |
|-----------------------|---|---|-----------|--|
| Qy | 249 | ESSECIKLKWSIPGLPIPARCFDYEIEIREDDTTLVTATVENETYILKTTNETRQLCFVY | 308 | ESSECIKLKWSIPGLPIPARCFDYEIEIREDDTTLVTATVENETYILKTTNETRQLCFVY |
| Db | 250 | EGT-RLSTQWEKPVSAFFIHCFDYEVKIHNRNGYLQIEKLMNFAFISIIDLSKDYDVQV | 309 | EGT-RLSTQWEKPVSAFFIHCFDYEVKIHNRNGYLQIEKLMNFAFISIIDLSKDYDVQV |
| Qy | 309 | RSKNYICSDGDIWSESDKQCEGDELSKTKTLRFLWPGFTILILVFTVGLLL 363 | 309 | RSKNYICSDGDIWSESDKQCEGDELSKTKTLRFLWPGFTILILVFTVGLLL 363 |
| Db | 309 | RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILL 356 | 309 | RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILL 356 |
| RESULT | 3 | | | |
| Q14631 | | | | |
| ID | Q14631 | PRELIMINARY; | PRT; | 396 AA. |
| AC | Q14631; | | | |
| DT | 01-NOV-1996 (Tremblrel. 01, Created) | | | |
| DT | 01-NOV-1996 (Tremblrel. 01, Last sequence update) | | | |
| DT | 01-MAR-2001 (Tremblrel. 16, Last annotation update) | | | |
| DE | INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR. | | | |
| GN | HSIL5R2. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=PERIPHERAL BLOOD; | | | |
| RX | MEDLINE=92121815; PubMed=1732409; | | | |
| RA | Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.; | | | |
| RX | "Molecular cloning and expression of the human interleukin 5 | | | |
| RT | receptor.; | | | |
| RL | J. Exp. Med. 175:341-351(1992). | | | |
| DR | EMBL; X61177; CAA43484.1; - | | | |
| DR | InterPro; IPR002996; - | | | |
| DR | InterPro; IPR003532; - | | | |
| DR | PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1. | | | |
| KW | Signal. | | | |
| FT | SIGNAL | 1 | 20 | POTENTIAL. |
| FT | CHAIN | 21 | 396 | INTERLEUKIN-5 RECEPTOR TYPE 2. |
| SEQ | SEQUENCE | 396 AA; | 44998 MW; | LAB60619842ACDA5 CRC64; |
| Query Match | 14.8%; | Score | 309.5; | DB 4; Length 396; |
| Best local Similarity | 27.6%; | Pred. No. | 1.3e-19; | |
| Matches | 98; | Conservative | 65; | Mismatches 151; Indels 41; Gaps |
| Qy | 27 | DTEIKVAPRODFEIVDPGYLGLYLQWQPPILSDHDKRECTVEYELKYRNGISFTWYTIIT 86 | | |
| Db | 25 | DEKISLPPVNTTKVTG-LAQVLLQWKPDDQEQ-RNVLEYQVKNAPKEDDYETRIIT 82 | | |
| Qy | 87 | KNLYKDGFDLNGKIEAKIHTLFPQWCTNGSEVQSSWAETTYWISQGPETKRVQDMCV 146 | | |
| Db | 83 | ES---KCVTILHKGFSAVRTILQ---NDHSLASSWASAEHL-APGSPGTSIVNLCT 135 | | |
| Qy | 147 | -----YYNQYLL-CSWRPGIGVLDTNYNLF-----WYGLDHALQCVDIKAD 191 | | |
| Db | 136 | TNTTWDNYSRLRSYQVSLHCTWLVTGTDPAEDTOFYLYRYGSWTE-----ECQEYSKDT 189 | | |
| Qy | 192 | -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYTFQLONTVKEPLPPVYLTFTR 248 | | |
| Db | 190 | LGRNIACWFRPTFLSLKGRDLAVLVNGSSKHSNAIRPFDQLFAHLDQNPPLNVAETAI 249 | | |
| Qy | 249 | ESSECIKLKWSIPGLPIPARCFDYEIEIREDDTTLVTATVENETYILKTTNETRQLCFVY 308 | | |
| Db | 250 | EGT-RLSTQWEKPVSAFFIHCFDYEVKIHNRNGYLQIEKLMNFAFISIIDLSKDYDVQV 308 | | |
| Qy | 309 | RSKNYICSDGDIWSESDKQCEGDELSKTKTLRFLWPGFTILILVFTVGLLL 363 | | |
| Db | 309 | RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILL 356 | | |
| RESULT | 4 | | | |
| Q15469 | | | | |
| ID | Q15469 | PRELIMINARY; | PRT; | 333 AA. |
| AC | Q15469; | | | |

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSIL5RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
  receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL: X62156; CAA44081.1; -.
DR InterPro; IPR002996; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT SIGNAL 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 14.0%; Score 292; DB 4; Length 333;
Best Local Similarity 28.0%; Pred. No. 3.9e-18;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPQDFEIVDPGYLYLQWQPPSLDHFKECTVEYELKYNIGSETWTKTIT 86
Db DEKISLPPVNTIKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
QY 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVOSSAETTYWISPOGIPETKVQDMDCV 146
Db ES-----KCVTLHKGFSAVSRTILO---NDHSLASSASAEHL-APPGSPGTSIVNLTCT 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGLDHALQCVDIYKAD 191
Db TTTEDNYSRLRSYQVSLHCWLVGTDAPEDTQYFLYRGSWTE-----ECQEYSKDT 189
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNIVKPLPPVYLAFTR 248
Db LGRNIACWFPRTILSKGRDLAVLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPICPARCFDYEIIEIREDDTLVATVENETTYLTKTNETROLQCFV 308
Db EGT-RLSIQWKEKPVSAFPIHCFDYEVIHTRNGYLQTEKILMTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGDIWSEWS 326
Db RAAVSMCREAGLWSEWS 326

RESULT 5
Q920K4 PRELIMINARY; PRT; 415 AA.
AC Q920K4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.
GN GPIL-5RA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Norris T.E.;
RT "Cloning and Characterization of the Guinea Pig Interleukin-5 receptor

```

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RT alpha cDNA.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U55215; AAD09361.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003532; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA.
SQ SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match 14.0%; Score 291.5; DB 11; Length 415;
Best Local Similarity 26.8%; Pred. No. 5.7e-18;
Matches 101; Conservative 65; Mismatches 160; Indels 51; Gaps 19;

QY 6 LAIGCLYTLFLISTTGTCTSSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLDHFKEC 65
Db ILGAIETLQDTL-----PDKRFLLLPPINFITKVTG-LAQVVLCEWPNPQGO-KNV 58
QY 66 TVEYELKYNIGSETWTKTITKNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVOSSWAE 125
Db NLNYHVKINTPQEDYE---TRNTQSKCETTLHQGSASVETIL-WH--GHSLLASSWVS 112
QY 126 TTYWISPGQIPETKVQDMDCV-----YNNQW---YLLCSWKPGIGVLLDTNLYF- 173
Db AEH-KAPPGSPGTSIVNLTCTNTAASNYNLKSYEVLHCTWLAGKADPEDTQYFLYR 171
QY 174 ---WYEGLDHALQCVDIYKAD-GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSY 227
Db YGPWTE-----ECQEYSKDTLSRNTACWFPRTFTHSKARDRLAVHNGSSNHATIKPFD 225
QY 228 FTQIQNIVKPLPPVYLFTFTRESSCEIKLWSIPLGPICPARCFDYEIETI-REDDTTLVTA 286
Db QLEDTQALDQNPMDVTAETEGS-RLSIQWKEKPVSAFPIHCFEYEVKICNTKDYQYQEK 284
QY 287 TVENETTYLTKTNETROLQCFVVRVNIYCSDDGDIWSEWSKQWEGEDLSKTKLLRFLWL 346
Db TTTNA--FVSTTGVGSYISQVRAAVSPHCRAMGLWSKWS-OPVTVGKE--KKIAGWFL 339
QY 347 -----PFGFILILVIFV 358
Db ITLTAVLCFILLIIFFL 356

RESULT 6
O97597 PRELIMINARY; PRT; 349 AA.
AC O97597;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.L., Hirano A., Brown W.C., Estes D.M.;
RT "Biological activities of interleukin-13 on bovine lymphocytes:
  implications for signaling through IL-13Ralpha.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF074402; AAC98147.1; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003532; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1

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FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 12.7%; Score 264.5; DB 6; Length 349;
Best Local Similarity 24.4%; Pred. No. 1.2e-15;
Matches 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;

QY 53 WOPPLSLDHFKECTVEYELKYRNTGSETWKTITKNLHYKDGFDLNLKGIEAKIHTLLPWQ 112
Db 18 WNPPEGAS--PNCISLKY---FSGNGKQDKKIAPET-HRSKEVPLNERICLQVGS-----Q 67

QY 113 C-TNGSEVQSSWAETTYWISQIPETKQVDMDCVYNNQWYLLCSWPKGIGVLDITNYNL 171
Db 68 CSTNESEKPSILVEKCF-SPEGDPESAVTALQCIWHLNRYMKCTWLPGRNASDPNXYL 126

QY 172 FYWTEGLDHALQVDYIKADQNTGCRFPYLEASD--YKDFYICVNGSSSENKPIRSYFT 229
Db 127 YWHSNLGKILQCNFYR-EGQHIACSFNLTWKVDSSFEQHSVQVMVRDNAGKISPSFNI 185

QY 230 FOLQNIKVPPLPPVLTFTRESSCEIKLKWISPLGPIPARCFDYIEIREDDTTTLVTATVE 289
Db 186 VPLSHVKP-DPSHIKNLSFONGDLYQWNTPNQ-FOSQCLCYEVEVINSHA----- 235

QY 290 NETYLTNTNTR-----QLCFVV-----RSKVNIYC-SDDGIWS 323
Db 236 -ETHDIEFYEAQKQNTFEGLNLTGTCFMPVPGVLPDLTNTVIRVKTNKLCEYEDDKLWS 294

QY 324 EWSDKQCEGEDLSKKLLRFLWLPFGFILLIVFTGLLL 363
Db 295 NWS-----QAMSIGOKANQTFYIT--TLLIIPVIVAAVI 327

RESULT 7
Q9UDY5 PRELIMINARY; PRT; 279 AA.
AC Q9UDY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81380; AAD00511.2; -
DR HSP; P40189; I8QU.
DR InterPro; IPR002996; -
DR InterPro; IPR003532; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;

Query Match 11.6%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 1e-13;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;

QY 11 LYTFELISTFECTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLDHFKECTVEY- 69
Db 10 LWALLLCAGGSGGGGAAPTETQPPVTNLSVSNELCTVIWNPPEGAS--SNCSLWYF 67

QY 70 ----ELKYRIGSTWKTITKNLHYKDGFDLNLKGIEAKIHTLLPWQ--TNGSEVQSSWA 124
Db 68 SHFGDKQDKKIAPETRSI-----EVLPLNERICLQVGS-----QCSNESEKPSILV 114

QY 125 ETTTWIS-POGIPETKQVDMDCVYNNQWYLLCSWPKGIGVLDITNYNLFYWTEGLDHALQ 183
Db 115 EKC--ISPPEGDPESAVTELQCIWHLNLSYMKCSWLPGRNTSPDNTYLYYHRSLEKIHQ 172
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QY 184 CVDYIKADQNIKGRFPYLEASD--YKDFYICVNGSSSENKPIRSYFTFOLQNIKVLPP 241
Db 173 C-ENIFREGQYFCGSDLTWKVDSSFEQHSVQIMVKDNAGKIRPSFNIVPLTSRVKPDPP 231

QY 242 --VYLTFTRESSCEIKLKWISPLGPIPARCFDYIEIREDDT 281
Db 232 HIKNLSPHND--DLVYQWENPQNF-SRCLFYEVEVNNST 269

RESULT 8
Q9DEQ1 PRELIMINARY; PRT; 363 AA.
AC Q9DEQ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN SEQUENCE FROM N.A.
RA Wang T., Secombes C.J.;
RL "Cloning and expression of the first non-mammalian cytokine receptor
common gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1; -
KW Receptor.
FT NON_TER
SQ SEQUENCE 363 AA; 41861 MW; DF69B2EB3EEA06D3 CRC64;

Query Match 9.5%; Score 197.5; DB 13; Length 363;
Best Local Similarity 21.9%; Pred. No. 1.2e-09;
Matches 61; Conservative 56; Mismatches 134; Indels 27; Gaps 9;

QY 97 LNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISQIPETKQVDMDCVYNNQWYLLCS 156
Db 1 IHKVRVELVTIPTVTHFDKMGVSW--LFLISLOGYEAPSTPNVNLINDYVNCI 58

QY 157 WKPGIGVLLDTNLYWIEGLDHALQVDYIKADQNIKGRFPYLEASDYKDFYICVNG 216
Db 59 WSE--QSIPEVNTFFSSRIKDNMECTTYLQESYAVGCLSYDKSDRFR----- 108

QY 217 SSENKPIRSYFTFQ---LQNIKVPPLPPVLTFTRESSCEIKLKWISPLGPIPARCFDYE 273
Db 109 TLTKLVHQNMSYVQDHNLSWKLYPPVNLSEVMNKDPELNLYNNKNTF---CIESE 165

QY 274 IEIREDDTTLTATVENE-TYTLKTTNETRQLCFVRSKVNICYGDDGIWSEWSDKQWE 332
Db 166 VRYRINDKWKTSPTSKEQYAVAPFLKSSRYEFQVAVRVDNMDGCESEFWSEWSQIQWD 225

QY 333 G-----EDLSKTLRLFWLP-FGFIILIVFTGLLL 363
Db 226 SMKGNNTDISGSS-MSVWKPVLSLVGMTLFIACML 262

RESULT 9
Q9PT10 PRELIMINARY; PRT; 611 AA.
AC Q9PT10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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RN  SEQUENCE FROM N.A.
RP  MEDLINE=20087225; PubMed=10618394;
RX  Huang H., Brown D.D.;
RA  "Prolactin is not a juvenile hormone in xenopus laevis
RT  metamorphosis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR  EMBL; AF193800; AAF05776.1; -
DR  HSP; P16471; 1BP3.
DR  InterPro; IPR001777; -
DR  InterPro; IPR002996; -
DR  InterPro; IPR003528; -
DR  Pfam; PF00041; fn3; 1.
DR  SMART; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR  Receptor.
KW  SMART; SM00060; FN3; 1.
SQ  SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;

Query Match      8.9%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY  127 TYWISPGQIPETKVQDMCVYNNQYLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCV 186
    | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKNKPGSDGLPTNYSLLYRKENDPKIYEC 80

QY  187 YIKADGQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTQLQNIKPL 239
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  81 YV-TSGLN-SCFFDKAHTSFWIFYHIYVYNNATNALGSNVSDSESDVTY-----IVQPY 131

QY  240 PPVYLTTRESS-CEIKLKWISPLGPIPARCFD-----YEIEIREDDTTLVTATVE 289
    | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  132 PPTNVSLAVESGHDLKWK-----LPPAMVDVQSGWLTLYKYEVRYKEEQEWEAHLV 185

QY  290 NETYTLKTTNETQLCFVVRKSVNIYCS-DDGIWSEWSDKOCWEGEDLSKTLRLFWLPF 348
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  186 GNQLKLKLFGLTPGNGYVQ----VRCKPDSGHWSEWSTESYIQIPGGKKKTDLTWISI 241

QY  349 GFILLIVFVT 359
    | | | | | | | |
Db  242 G-ALSAVICLT 251

RESULT 11
Q64146
ID  Q64146 PRELIMINARY; PRT; 896 AA.
AC  Q64146;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE  01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE  INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN  RIL-3R<BETA>.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=95370942; PubMed=7643220;
RA  Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT  "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT  microglia and its mRNA expression in vivo.";
RL  J. Neurosci. 15:5800-5809(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=WISTAR; TISSUE=BRAIN;
RC  Gebicke-Haerter P.J.;
RL  Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; S79263; AAB35068.1; -.
DR  EMBL; AJ000555; CAA04186.1; -.
DR  InterPro; IPR000282; -.
DR  InterPro; IPR001777; -.
DR  InterPro; IPR002996; -.
DR  InterPro; IPR003531; -.
DR  Pfam; PF00041; fn3; 2.
DR  PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR  SMART; SM00060; FN3; 1.
KW  Signal.
FT  NON_TER 1 896
FT  NON_TER 896
SQ  SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match      8.5%; Score 178; DB 11; Length 896;
Best Local Similarity 21.4%; Pred. No. 2e-07;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY  5 CLAIGCL--YT-FLISTTFGCTSSSDTEIKVN-----PPQDFEIVDPGYLGLV 49
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  94 CVPRCVLPYTFQFSVKEDYYSLQPDRLSLHLVPLAQHVQPPPPKDISPSG--DHF 151

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=20087225; PubMed=10618394;
RX  Huang H., Brown D.D.;
RA  "Prolactin is not a juvenile hormone in xenopus laevis
RT  metamorphosis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR  EMBL; AF193800; AAF05776.1; -
DR  HSP; P16471; 1BP3.
DR  InterPro; IPR001777; -
DR  InterPro; IPR002996; -
DR  InterPro; IPR003528; -
DR  Pfam; PF00041; fn3; 1.
DR  SMART; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR  Receptor.
KW  SMART; SM00060; FN3; 1.
SQ  SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;

Query Match      8.9%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY  127 TYWISPGQIPETKVQDMCVYNNQYLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCV 186
    | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKNKPGSDGLPTNYSLLYRKENDPKIYEC 80

QY  187 YIKADGQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTQLQNIKPL 239
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  81 YV-TSGLN-SCFFDKAHTSFWIFYHIYVYNNATNALGSNVSDSESDVTY-----IVQPY 131

QY  240 PPVYLTTRESS-CEIKLKWISPLGPIPARCFD-----YEIEIREDDTTLVTATVE 289
    | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  132 PPTNVSLAVESGHDLKWK-----LPPAMVDVQSGWLTLYKYEVRYKEEQEWEAHLV 185

QY  290 NETYTLKTTNETQLCFVVRKSVNIYCS-DDGIWSEWSDKOCWEGEDLSKTLRLFWLPF 348
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  186 GNQLKLKLFGLTPGNGYVQ----VRCKPDSGHWSEWSTESYIQIPGGKKKTDLTWISI 241

QY  349 GFILLIVFVT 359
    | | | | | | | |
Db  242 G-ALSAVICLT 251

RESULT 10
Q9IBF6
ID  Q9IBF6 PRELIMINARY; PRT; 611 AA.
AC  Q9IBF6;
DT  01-OCT-2000 (TrEMBLrel. 15, Created)
DT  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE  01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE  PROLACTIN RECEPTOR.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
RT  "Cloning of a cDNA for xenopus prolactin receptor and its
RT  metamorphic expression profile.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB030443; BAA90400.1; -.
DR  InterPro; IPR001777; -.
DR  InterPro; IPR002996; -.
DR  Pfam; PF00041; fn3; 1.
DR  PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR  SMART; SM00060; FN3; 1.
KW  Receptor.
SQ  SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:05:53 ; Search time 60.7 Seconds
(without alignments)
379.524 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: 2104

Sequence: 1 MAVFCLAIGCLYFLISTTF.....LLLRKPNTPYKMIPEFFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|--------------------|
| 1 | 2104 | 100.0 | 380 | 18 | Human interleukin- |
| 2 | 2104 | 100.0 | 380 | 18 | Human IL-13 bindin |
| 3 | 2104 | 100.0 | 380 | 18 | Human Zcytor2 cyto |
| 4 | 2104 | 100.0 | 380 | 19 | Human HR-1 recepto |
| 5 | 2104 | 100.0 | 380 | 19 | Human cytokine/pep |
| 6 | 2104 | 100.0 | 380 | 19 | Human sapiens HR-1 |
| 7 | 2104 | 100.0 | 380 | 21 | IL-13 binding chai |
| 8 | 2104 | 100.0 | 380 | 22 | Human interleukin |
| 9 | 2104 | 100.0 | 380 | 22 | Human IL-13 recept |
| 10 | 2078 | 98.8 | 380 | 18 | Human Zcytor2 cyto |
| 11 | 1853 | 88.1 | 372 | 18 | Celebus macaque Zc |

| | | | | | | |
|----|--------|------|------|----|----------|--------------------|
| 12 | 1753 | 83.3 | 315 | 19 | AAW56261 | Mature interleukin |
| 13 | 1753 | 83.3 | 359 | 19 | AAW56260 | Construct containi |
| 14 | 1194.5 | 56.8 | 383 | 18 | AAW35294 | Murine IL-13 bindi |
| 15 | 1194.5 | 56.8 | 383 | 21 | AAW52595 | IL-13 binding chai |
| 16 | 1194.5 | 56.8 | 383 | 22 | AAW72135 | Murine interleukin |
| 17 | 1194.5 | 56.8 | 383 | 22 | AAW29747 | Mouse IL-13 recept |
| 18 | 456 | 21.7 | 157 | 19 | AAW56252 | Interleukin-13 bin |
| 19 | 311.5 | 14.8 | 396 | 13 | AAW22216 | Sequence of human |
| 20 | 311.5 | 14.8 | 396 | 13 | AAW22220 | Sequence of secret |
| 21 | 311.5 | 14.8 | 420 | 13 | AAW22219 | Human interleukin- |
| 22 | 311.5 | 14.8 | 420 | 13 | AAW82842 | Human IL-5 recepto |
| 23 | 310.5 | 14.8 | 421 | 13 | AAW25064 | Sequence of human |
| 24 | 305.5 | 14.5 | 420 | 13 | AAW22215 | Protein used in pr |
| 25 | 297 | 14.1 | 313 | 18 | AAW21856 | Mouse interleukin- |
| 26 | 296 | 14.1 | 426 | 18 | AAW09821 | Human interleukin- |
| 27 | 295.5 | 14.0 | 427 | 18 | AAW24973 | Human interleukin- |
| 28 | 295.5 | 14.0 | 427 | 22 | AAW19807 | Human interleukin- |
| 29 | 294.5 | 14.0 | 426 | 18 | AAW09822 | IL5-R-GBP 130 fusi |
| 30 | 292.5 | 13.9 | 1026 | 16 | AAW70121 | Soluble human IL-5 |
| 31 | 292 | 13.9 | 335 | 13 | AAW25063 | shIL-5R-alpha. Sy |
| 32 | 292 | 13.9 | 335 | 14 | AAW33699 | Human interleukin- |
| 33 | 286.5 | 13.6 | 427 | 22 | AAW19808 | IL-13/IL-4 dual tr |
| 34 | 285 | 13.5 | 793 | 21 | AAW92208 | IL-13/IL-4 dual tr |
| 35 | 249.5 | 11.9 | 155 | 19 | AAW56255 | Sequence of interl |
| 36 | 248 | 11.8 | 398 | 13 | AAW22212 | Sequence of interl |
| 37 | 247 | 11.7 | 415 | 13 | AAW22211 | Sequence of interl |
| 38 | 247 | 11.7 | 415 | 13 | AAW22217 | Sequence of interl |
| 39 | 229 | 10.9 | 332 | 13 | AAW22213 | Sequence of interl |
| 40 | 229 | 10.9 | 332 | 13 | AAW22213 | Sequence of interl |
| 41 | 229 | 10.9 | 332 | 13 | AAW22213 | Sequence of interl |
| 42 | 229 | 10.9 | 332 | 13 | AAW22213 | Sequence of interl |
| 43 | 220 | 10.5 | 369 | 15 | AAW47148 | IL-2 receptor gamm |
| 44 | 219 | 10.4 | 347 | 15 | AAW47149 | IL-2 receptor gamm |
| 45 | 209.5 | 10.0 | 369 | 15 | AAW59094 | Murine IL-2R gamma |

ALIGNMENTS

| | |
|----------|--|
| RESULT | 1 |
| AAW24972 | ID AAW24972 standard; protein; 380 AA. |
| XX | AC AAW24972; |
| XX | AC AAW24972; |
| XX | DT 22-JUN-1998 (first entry) |
| XX | DE Human interleukin-13 beta receptor. |
| XX | DE Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13. |
| XX | OS Homo sapiens. |
| XX | XX W09720926-A1. |
| XX | XX 12-JUN-1997. |
| XX | XX 07-NOV-1996; 96WO-FR01756. |
| XX | XX 06-DEC-1995; 95FR-0014424. |
| XX | XX (SNFI) SANOFI SA. |
| XX | XX Caput D, Ferrara P, Laurent P, Vita N; |
| XX | XX WPI; 1997-319773/29. |
| XX | XX N-PSDB; AAT85826, AAT86464. |
| XX | XX New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy, etc |
| XX | XX Claim 1; Figure 2a; 83pp; French. |

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunoassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPPLSLD 60
 Db 1 mafvclaigcltyflistftgctssdteikvnpqdfvdpvglylylqwpplsl 60

Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlhykdgfdlnkgleakihltllpwqctngse 120

Qy 121 SSWAETTYWISPGIPETKVDQMCVYNNWQYLICSWKPGIGVLLDTNLYFWYEGLDH 180
 Db 121 sswaettywispipetkvdqmcvynnwqyllicswkpgigvlltdtnlyfwyegldh 180

Qy 181 ALQCVDYIKADQNGICRFPYLEASDKDFYICVNGSENKPIRSSYFTFQQLNIVRPLP 240
 Db 181 alqcvdyikadqngicrfyleasdkdfyicvngsenkpirssyftfqlnivrplp 240

Qy 241 PVLFTFRESSCEIKLWSIPGLPIPARCFDYEIEIREDDTTLVTAVENETYILKTTNE 300
 Db 241 pvlftfressceiklwsipglpmparcfdyeiireddtllvtatvenetyilktne 300

Qy 301 TROLCFVVRKVNLYCSDGGLWSWSKQCEWGEDLSKTLLEWLPFGFTLLILVIFVTG 360
 Db 301 trqlcfvvrkvnlycsdggllwsesdkqcewedlskttlrlwlpfgftllilvifvtg 360

Qy 361 LLRLKPNTPYKMIPEFFCDT 380
 Db 361 llrlkpntpykmipeffcdt 380

RESULT 2
 AAW35295
 ID AAW35295 standard; Protein; 380 AA.

XX AAW35295;
 AC
 XX
 DT 27-MAR-1998 (first entry)
 XX Human IL-13 binding chain of the IL-13 receptor.
 DE Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= signal_sequence
 FT /note= "putative"
 FT 26..380
 FT Protein
 FT /label= mature_protein
 FT 26..341
 FT Domain
 FT /label= extracellular_domain
 FT 342..362
 FT Domain
 FT /label= transmembrane_domain
 FT 363..380
 FT Domain
 FT /label= intracellular_domain

XX WO9731946-A1.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-US03124.

XX 01-MAR-1996; 96US-0609572.

XX (GEMY) GENETICS INST INC.

XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;

XX WPI; 1997-448632/41.

DR N-PSDB; AAT95214.

XX New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis

XX Claim 11; Pages 34-35; 49pp; English.

XX The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.

XX Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPPLSLD 60

Db 1 mafvclaigcltyflistftgctssdteikvnpqdfvdpvglylylqwpplsl 60

Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120

Db 61 hfkectveyelkynigsetwktitknlhykdgfdlnkgleakihltllpwqctngse 120

Qy 121 SSWAETTYWISPGIPETKVDQMCVYNNWQYLICSWKPGIGVLLDTNLYFWYEGLDH 180

Db 121 sswaettywispipetkvdqmcvynnwqyllicswkpgigvlltdtnlyfwyegldh 180

QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngsenkpirssyftfqlqnvkplp 240
 QY 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYETIREDDTLTATVENETYTLKTTNE 300
 DB 241 pvyltftressceiklwsipglpmparcdyeteireddtltatvenetytlktne 300
 QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKTLRLFWLPFGFILLIVFVTG 360
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqwedlsktlrlfwlpfgfllilvifvtg 360
 QY 361 LLRLKPNTPYKMIPEFFCDT 380
 DB 361 llrlkpntpykmipecfcdt 380

RESULT 3
 AAW36613
 ID AAW36613 standard; Protein; 380 AA.
 XX
 AC AAW36613;
 DT 30-MAR-1998 (first entry)
 XX
 DE Human Zcytor2 cytokine receptor protein.
 XX
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 340..363
 FT /label= transmembrane_domain
 FT Domain 364..380
 FT /label= intracellular_domain
 FT Domain 25..339
 FT /label= ligand_binding_domain
 XX
 PN WO9733913-A1.
 XX
 XX 18-SEP-1997.
 XX
 PF 12-MAR-1997; 97WO-US04043.
 XX
 PR 13-MAR-1996; 96US-0013345.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 PI O'Hara PJ;
 XX
 XX WPI; 1997-470820/43.
 DR N-PSDB; AAT96782.
 XX
 XX New nucleic acid encoding testis-specific cytokine receptor - useful
 PT for identification of ligands or antagonists, potentially for use as
 PT male contraceptives or for infertility treatment
 XX
 PS Claim 2; Page 47-48; 79pp; English.
 XX
 CC This sequence represents a novel ligand-binding receptor, Zcytor2,
 CC which shares homology with cytokine receptors and was isolated from human
 CC placental polyA+ RNA. The resulting polypeptide is a receptor for
 CC cytokines (particularly interleukin-13) and is expressed on the surface
 CC of testicular cells, probably being involved in spermatogenesis. It can
 CC be used to detect ligands that promote proliferation and/or
 CC differentiation of such cells in cultures and may also be used to treat
 CC infertility. Antagonists of this receptor may be used to characterise
 CC ligand-receptor interactions and as male-specific contraceptives. By
 CC blocking the action of IL-13, receptor antagonists and ligand-binding
 CC this receptor can also be used to modulate immune function, e.g. in

CC allergy and asthma, as a diagnostic to determine circulating levels of
 CC ligand and also to isolate and purify ligands. Antibodies can be used to
 CC assay circulating receptor (an abnormal level may be indicative of
 CC disease such as cancer), for labelling cells that express the receptor,
 CC and therapeutically as antagonist.
 XX
 SQ Sequence 380 AA;
 Query Match 100.0%; Score 2104; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTFELISTTFCCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
 DB 1 mafvclaigcltyflisttfgctssdteikvnpqdfei vdp gyl gyl ylwqppisld 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITTNLHYKDFGFDLNGKIEAKIHLLPWCQTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktiitknlhykdgfdlnkgleakihtllpwqctngsevg 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQOYLCSWKPGIGVLLDTNYNLFYWEGLDH 180
 DB 121 sswaettywispgipeckvqdmcdvynnwqylylcskwpigvlldtnynlfywegldh 180
 QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngsenkpirssyftfqlqnvkplp 240
 QY 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYETIREDDTLTATVENETYTLKTTNE 300
 DB 241 pvyltftressceiklwsipglpmparcdyeteireddtltatvenetytlktne 300
 QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKTLRLFWLPFGFILLIVFVTG 360
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqwedlsktlrlfwlpfgfllilvifvtg 360
 QY 361 LLRLKPNTPYKMIPEFFCDT 380
 DB 361 llrlkpntpykmipecfcdt 380

RESULT 4
 AAW41520
 ID AAW41520 standard; Protein; 380 AA.
 XX
 AC AAW41520;
 XX
 DT 22-JUN-1998 (first entry)
 XX
 DE Human HR-1 receptor.
 XX
 KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
 KW haematopoietic disorder; tumour; therapy; diagnosis.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT Protein 22..380
 FT /label= Mat_protein
 XX
 PN WO9747741-A1.
 XX
 PD 18-DEC-1997.
 XX
 PF 12-JUN-1996; 96WO-US10262.
 XX
 PR 12-JUN-1996; 96WO-US10262.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Appelbaum ER, Hu J;
 XX WPI: 1998-052308/05.
 DR N-PSDB; AAV04131.
 XX Nucleic acid sequence encoding human cytokine peptide hormone
 PT receptor - useful to treat, prevent or diagnose, e.g. lowered
 PT resistance to infection, asthma, allergy or haematopoietic disease
 XX
 PS Claim 13; Page 62-64; 76pp; English.
 XX This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated the HR-1 receptor, that shows 27% identity
 CC and 52% similarity to the interleukin-5 receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
 CC human testis library. Recombinant HR-1 receptor can be expressed
 CC in claimed host cells, and used in a claimed method for identifying
 CC compounds which bind to, and activate or inhibit, it. HR-1
 CC receptor activators and agonists can be used to treat, prevent or
 CC diagnose predisposition to lowered resistance to infection, asthma,
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
 CC be used to treat conditions associated with HR-1 receptor
 CC overexpression. The antibodies can also be used to determine HR-1
 CC receptor levels, since overexpression may be diagnostic of tumours.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIAGCLYTLISTTFCGTSSTDEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
 Db 1 mafvclaiagcltytlsttfgtssstdeikvnpqdfelvdpgylylylqwqpplsl 60
 Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNKGEAKIHLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlykdgfdlnkgeakihllpwqctngse 120
 Qy 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
 Db 121 sswaettywispgipetkvqdmcvynnwqyllcswkpgigvlldtnlynlfywe 180
 Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSYFTFOLQNVKPLP 240
 Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkpirsyftfqlqnvkplp 240
 Qy 241 PVYLTFTRESSECEIKLWSIPGLPIPARCFDYEIEIREDDTTLVTAVENETYTLKTNE 300
 Db 241 pvyltftressceiklwsipglpigarcfdyeieireddtlvtavenetytlktne 300
 Qy 301 TRQLCFVVRKVNIVYCSDDGIWSEWSKQCEWGEDLSKKTLLRFLWLPFGFILLIVFVTG 360
 Db 301 trqlcfvvrkvnivycsddgiwsewsdkqcewedlskktllrflwlpfgfllivfvtg 360
 Qy 361 LLLRKNPTNPKMPEFFCDT 380
 Db 361 lllrkpntypkmpfeffcdt 380

RESULT 5
 AA41502
 ID AA41502 standard; Protein; 380 AA.

XX AA41502;
 AC
 XX
 DT 08-JUN-1998 (first entry)
 XX Human cytokine/peptide receptor, HR-1 receptor.

XX HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
 KW neutropaenia; therapy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..21
 FT Peptide /label= Sig_peptide
 FT Protein 22..380
 FT /label= Mat_protein
 FT /note= "Claim 14"
 XX EP812913-A2.
 XX 17-DEC-1997.
 XX 04-JUN-1997; 97EP-0303815.
 XX 12-JUN-1996; 96US-0017843.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX Appelbaum ER, Hu J;
 XX WPI: 1998-034974/04.
 DR N-PSDB; AAV04075.
 XX Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 XX
 PS Claim 13; Page 27-28; 34pp; English.

XX This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor. The amino acid sequence
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human
 CC testis cDNA library. It shows 27% amino acid identity and 52%
 CC similarity with the human interleukin-5 receptor. Also claimed are
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an
 CC antagonist to the polypeptide, antibody against the polypeptide, an
 CC antagonist that inhibits the activity of the polypeptide, a process
 CC for diagnosing a disease, or a susceptibility to disease, related
 CC to expression of HR-1 receptor, and a method for identifying
 CC compounds that activate or inhibit the HR-1 receptor. HR-1
 CC receptor protein and polynucleotides can be used for research,
 CC biological, diagnosis and (gene) therapy applications, e.g. to
 CC increase resistance to infections in individuals with trauma and/or
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropaenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.

XX Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIAGCLYTLISTTFCGTSSTDEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
 Db 1 mafvclaiagcltytlsttfgtssstdeikvnpqdfelvdpgylylylqwqpplsl 60
 Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNKGEAKIHLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlykdgfdlnkgeakihllpwqctngse 120
 Qy 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
 Db 121 sswaettywispgipetkvqdmcvynnwqyllcswkpgigvlldtnlynlfywe 180

Db 121 sswaettywispagipetkvqmdcvynwqyllcswkpgigvlltdnynlfwyegldh 180
QY 181 ALOCVDYIKADGONIGCRFFYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNIYKPLP 240
Db 181 alqcvdyikadgqncgrfyleasdykdfyicvngsssenkpirssyftfqlqniwklp 240
QY 241 PVLTFTRSSCEIKLWSPGLGPIPARCFDYEIEIREDDTTLVATVENETYLKTTNE 300
Db 241 pylvltftrssceiklwspglgpiparcfdeyleireddttlvatvenetylktne 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGDELSKTLIRFWLPFGFTILILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlsktilrflwlpfgfllilvifvtg 360
QY 361 LLRKPNTPYKMPIEFFCDT 380
Db 361 llirkpntypkmpieffcdt 380

RESULT 6
AAW33603
ID AAW33603 standard; Protein; 380 AA.
XX
AC AAW33603;
XX
DT 08-JUN-1998 (first entry)
DE Homo sapiens HR-1 receptor.
XX
KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;
KW syndrome; aplastic anaemia; neutropaenia; cancer treatment;
KW infection resistance; diagnosis; tumours; HR-1 receptor;
KW asthma; allergic; haematopoietic; disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
XX
PN W09747742-A1.
XX
PD 18-DEC-1997.
XX
PF 09-JUL-1996; 96WO-US11459.
XX
PR 12-JUN-1996; 96WO-US10262.
PR 12-JUN-1996; 96US-0017843.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI Appelbaum ER, Hu J;
XX
DR WPI; 1998-052309/05.
DR N-PSDB; AAV02295.
XX
PT DNA encoding human cytokine-peptide hormone receptor - useful for
PT treating preventing or diagnosing, e.g. lowered resistance to
PT infection, asthma, allergy, or haematopoietic disease
XX
PS Claim 15; Fig 1; 75pp; English.
XX
CC The sequence is that of the human cytokine/peptide hormone receptor
CC (HR-1 receptor). This, or it's activators or agonists, can be used to
CC treat, prevent or diagnose predisposition to lowered resistance to
CC infection, asthma, allergic or haematopoietic disorders, e.g. where
CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
CC neutropaenia or cytotoxic treatments for cancer. Antagonists of the
CC receptor, e.g. antibodies or fragments of it may be used to treat
CC conditions associated with overexpression of the HR-1 receptor, e.g.
CC those listed above. Antibodies may also be used to assay levels of HR-1
CC receptor, overexpression of which may be diagnostic of tumours, by usual

CC immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
CC for affinity purification of the HR-1 receptor.
SQ Sequence 380 AA;
Query Match 100.0%; Score 2104; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIAGCLYFLISTTFCGCTSSDTEIKVNPDPQFEIVDPCYLGLYLQWOPPLSLD 60
Db 1 marvclaiagcllyflisttfcgctssdteikvnpdpqfeivdpqylylylqwpplsl 60
QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHFTLLPWQCTNGSEVQ 120
Db 61 hfkectveyelkyrnigsetwktitknlykdgfdlنگكieakihtllpwqctngsevg 120
QY 121 SSWAETTYWISPOGIPETKVQMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
Db 121 sswaettywispqgipetkvqmdcvynwqyllcswkpgigvlltdnynlfwyegldh 180
QY 181 ALOCVDYIKADGONIGCRFFYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNIYKPLP 240
Db 181 alqcvdyikadgqncgrfyleasdykdfyicvngsssenkpirssyftfqlqniwklp 240
QY 241 PVLTFTRSSCEIKLWSPGLGPIPARCFDYEIEIREDDTTLVATVENETYLKTTNE 300
Db 241 pylvltftrssceiklwspglgpiparcfdeyleireddttlvatvenetylktne 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGDELSKTLIRFWLPFGFTILILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlsktilrflwlpfgfllilvifvtg 360
QY 361 LLRKPNTPYKMPIEFFCDT 380
Db 361 llirkpntypkmpieffcdt 380

RESULT 7
AAW33603
ID AAW33603 standard; Protein; 380 AA.
XX
AC AAW33603;
XX
DT 12-SEP-2000 (first entry)
DE IL-13 binding chain of human IL-13 receptor.
XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; anti-allergic;
KW anti-inflammatory; antiasthmatic; vaccine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25 "signal peptide"
FT Protein 26..380
FT /note= "mature protein"
FT Domain 26..341
FT /note= "extracellular domain; a polypeptide
FT comprising amino acids 22-334 is
FT specifically claimed in Claim 11(e)"
FT Domain 342..362
FT /note= "transmembrane domain"
FT Domain 363..380
FT /note= "intracellular domain; a polypeptide
FT comprising amino acids 257-383 is
FT specifically claimed in Claim 11(f)"
XX

PN WO200036103-A1.
XX 22-JUN-2000.
XX 13-DEC-1999; 99WO-US29493.
XX 14-DEC-1998; 98US-0211335.
XX (GEMY) GENETICS INST INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
XX Wills-Karp M;
XX WPI: 2000-431587/37.
XX N-PSDB; AAA27912.
XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
XX an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
XX asthma, Grave's disease and inflammatory conditions of the lung -
XX Claim 11(d); Page 53-54; 60pp; English.
XX The present sequence is that of the interleukin-13 binding chain
XX (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
XX human testis cDNA clone (see AAA27912). IL-13bc is a member of
XX the haematopoietin receptor family that acts as a mediator of
XX IL-13. The invention provides methods for the recombinant
XX production of IL-13bc polypeptides, including claimed full-length
XX IL-13bc, its extracellular domain, and its intracellular domain.
XX IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
XX and IL-13 receptor inhibitors (e.g. antagonists of the interaction
XX of IL-13 and its receptor) can be used to treat conditions in
XX which IL-13 is implicated, particularly IgE-mediated conditions and
XX diseases including atopy, allergy, asthma, immune complex diseases
XX (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
XX thyroiditis and Grave's disease), lung inflammation,
XX immunodeficiency, and cancer. Since IL-13 inhibits macrophage
XX activation, IL-13bc proteins can also be used to enhance macrophage
XX activation, e.g. in vaccination, treatment of mycobacterial or
XX intracellular organisms or parasite infections. IL-13bc proteins
XX may also be used to potentiate the effects of IL-13 in vitro and
XX in vivo, as diagnostic agents, and to screen for agents capable of
XX binding to IL-13bc or IL-13 receptor, or which interfere with the
XX binding of IL-13 to its receptor.
XX SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 21; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIAGCLYFLISTTGTCTSSSTTEIKVNPQDFEIVDPGVLGYLYLQWQPLSLD 60
Db 1 mafvclaiagclytflisttgtctssstteikvnpqdfelvdpvglylylqwpplsl 60
QY 61 HFKECTVEYELKYNIGSEWTKLITKNLHYKDGFDLNGKIEAKIHTLLPWCQTNSEVQ 120
Db 61 hfkectveyelkynigsewtklittknlykdgfdlنگكieakihtllpwcqtnsevg 120
QY 121 SSWAETTYWISPOGIPETKVDQDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
Db 121 sswaettywispogipetkvdqdcvynnyqyllcswkpgigvllدtnlynlfywegl 180
QY 181 ALQCDVIKADGQNGICRFRFYLEADSKDYICVNGSSSENKPIRSSYFTFQQLNIVKPLP 240
Db 181 alqcdvikaadgngicrfrfyleadskdyicvngsssenkpirssyftfqlnivkpl 240
QY 241 PVIYTFRESSCEIKLKWSPICLPICAPCFDYEIREDDTTLVTATVENETYLKTTNE 300
Db 241 pviytfressceiklkwspiclpicapcfdyeireddttlvtatvenetylktne 300

QY 301 TROLCFVVRKVNIVCSDGSIWSEWSDKQWEGEDLSKTLRLFWLPFGFILLIVFVTG 360
Db 301 trqlcfvvrskvnivcsddgiwsewskqwegedskskllrlfwlpfgfllilvfv 360
QY 361 LLDRKPNNTYPRKMIPEFFCDT 380
Db 361 llldrknptypkmipecfcdt 380
RESULT 8
AA72136
ID AAY72136 standard; Protein; 380 AA.
XX
XX AAY72136;
XX 24-APR-2001 (first entry)
XX Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
XX Human; IL-13: interleukin-13 binding chain of IL-13 receptor; IL13bc;
XX therapy; tissue fibrosis; Schistosoma infection; surgical incision;
XX cyostatic; wound; IL-13 related condition; allergic condition;
XX nephrotic syndrome; thyroiditis; Grave's disease; cancer;
XX macrophage activation.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..25 /label= Signal_peptide
XX Region 1..81 /note= "This region is identical to the translated
XX sequence of an expressed sequence tag (EST) identified
XX as y999f10.rl human cDNA clone 41648 5"
XX Protein 26..380 /label= Mature_human_interleukin (IL)-13_binding_chain_
XX of_IL-13_receptor
XX Domain 26..341 /note= "Extracellular domain; this region is specifically
XX claimed in claims 1e, 6e, 15e and 23e"
XX Domain 342..362 /note= "Transmembrane domain"
XX Domain 363..380 /note= "Intracellular domain; this region is specifically
XX claimed in claims 1f, 6f, 15f and 23f"
XX
XX PN WO200078336-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-US17103.
XX 21-JUN-1999; 99US-0334512.
XX (GEMY) GENETICS INST INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
XX Wills-Karp M;
XX WPI: 2001-080753/09.
XX N-PSDB; AAD02335.
XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
XX in a mammalian subject, involves administering a pharmaceutical
XX composition comprising IL-13 antagonist -
XX Claim 1a; Page 69-70; 72pp; English.
XX The invention relates to a method of treating, or inhibiting
XX the formation of tissue fibrosis in mammals, which involves
XX administering a pharmaceutical composition comprising interleukin
XX (IL)-13 antagonist. The protein of the invention is useful for

CC treating tissue fibrosis resulting from infection with Schistosoma
CC or from healing of a wound which is a surgical incision, or
CC inhibiting formation of tissue fibrosis which affects tissues such
CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
CC biliary tract and gut. It is also used in the treatment or modulation
CC of various IL-13 related conditions such as allergic conditions,
CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
CC The present sequence is human interleukin (IL)-13
CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
CC to potentiate the effects of IL-13. This protein is also used to
CC enhance macrophage activation and hence can be used in vaccination
CC or treatment of mycobacterial or parasitic infections.
XX
XX
SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 22; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLYTLFISTFGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
DB 1 mafvclaigclytlfistfgctssdteikvnpqdfelvdpgvlylqwgppslid 60
QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
DB 61 hfkectveyelkyrnigsetwktitknhykdgfdlnkgeakhtlilpwqctngsevg 120
QY 121 SSWAETTYWISPGIPETPKVQDMDCVYVNWQYLLCSWKPGIGVLDTNLYNFYWEGLDH 180
DB 121 sswaettywispggipetkvdqmdcvynwqyllcswkpgigvlltdnynlfywegldh 180
QY 181 ALQCVDYIKADGQNGICRFPVLEASDYKDFYICVNGSENKPIRSSYTFQLOIVKPLP 240
DB 181 alqcvdyikadgngicrfpyleasdykdfyicvngssenkprrssytfqlqnvkplp 240
QY 241 PVYLFTRESSCEIKLWSIPLGPPIRCFDFYEIRDDDTLVATVENETYTLKTNE 300
DB 241 pvyilftressceiklwsiplgpiparcfdyeieirdddtlvtatvenetytlktne 300
QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQCWEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
DB 301 trqlcfvvrskvniycsddgiwsewsdkqcwgedlskktllrflwlpfgfillilvifvtg 360
QY 361 LLRLKPNTPYKMIPEFFCDT 380
DB 361 llrlkpntpkmipeffcdt 380

RESULT 9
AAB29748
ID AAB29748 standard; Protein; 380 AA.

XX AAB29748;

XX 23-FEB-2001 (first entry)

DE Human IL-13 receptor IL-13 binding chain (IL-13bc).

XX Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnery;
KW wound healing; schistosoma infection; liver; skin; muscle;
KW cartilage; cardiac tissue; lung tissue; uterine tissue;
KW intestinal tissue; vascular tissue; neural tissue.

OS Homo sapiens.

XX WO20006494-A1.

XX 02-NOV-2000.

XX

PF 28-APR-2000; 2000WO-US11612.
XX
PR 28-APR-1999; 99US-0301808.
XX
PA (GEMY) GENETICS INST INC.
XX
XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
PI Whitters MJ, Wood C;
XX
XX WPI: 2001-024676/03.
DR N-PSDB; AAC81416.
XX
PT Treating or inhibiting tissue fibrosis resulting from infection with
PT schistosoma and wound healing involves administering interleukin-13 or
PT interleukin-4 antagonist
XX
PS Claim 1; Page 76-77; 82pp; English.
XX

CC The invention relates to a method of treating fibrosis in a mammal
CC by administering an interleukin-13 (IL-13) antagonist or an IL-4
CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding
CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or
CC soluble fragments thereof. The method is useful for treating or
CC inhibiting the formation of tissue fibrosis resulting from the healing
CC of a wound, including a surgical incision wound, or from infection with
CC schistosoma. The method may be used to treat fibrosis in a variety of
CC tissues, particularly liver tissue, but also skin epidermis, skin
CC endodermis, muscle, tendon, cartilage, cardiac tissue, pancreatic
CC tissue, lung tissue, uterine tissue, neural tissue, pancreas,
CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
CC tissue. The present sequence represents human IL-13bc.
XX
SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 22; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLYTLFISTFGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
DB 1 mafvclaigclytlfistfgctssdteikvnpqdfelvdpgvlylqwgppslid 60
QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
DB 61 hfkectveyelkyrnigsetwktitknhykdgfdlnkgeakhtlilpwqctngsevg 120
QY 121 SSWAETTYWISPGIPETPKVQDMDCVYVNWQYLLCSWKPGIGVLDTNLYNFYWEGLDH 180
DB 121 sswaettywispggipetkvdqmdcvynwqyllcswkpgigvlltdnynlfywegldh 180
QY 181 ALQCVDYIKADGQNGICRFPVLEASDYKDFYICVNGSENKPIRSSYTFQLOIVKPLP 240
DB 181 alqcvdyikadgngicrfpyleasdykdfyicvngssenkprrssytfqlqnvkplp 240
QY 241 PVYLFTRESSCEIKLWSIPLGPPIRCFDFYEIRDDDTLVATVENETYTLKTNE 300
DB 241 pvyilftressceiklwsiplgpiparcfdyeieirdddtlvtatvenetytlktne 300
QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQCWEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
DB 301 trqlcfvvrskvniycsddgiwsewsdkqcwgedlskktllrflwlpfgfillilvifvtg 360
QY 361 LLRLKPNTPYKMIPEFFCDT 380
DB 361 llrlkpntpkmipeffcdt 380

RESULT 10
AAW36614
ID AAW36614 standard; Protein; 380 AA.
XX
AC AAW36614;

XX 30-MAR-1998 (first entry)
 XX DT
 XX DE Human zcytor2 cytokine receptor protein.
 XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 XX OS Homo sapiens.
 XX PN WO9733913-A1.
 XX PD 18-SEP-1997.
 XX PF 12-MAR-1997; 97WO-US04043.
 XX PR 13-MAR-1996; 96US-0013345.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 XX PI O'Hara PJ;
 XX DR WPI; 1997-470820/43.
 XX DR N-PSDB; AAT96783.
 XX PS New nucleic acid encoding testis-specific cytokine receptor - useful
 XX PT for identification of ligands or antagonists, potentially for use as
 XX PT male contraceptives or for infertility treatment
 XX FT
 XX PS Claim 1; Page 51-53; 79pp; English.
 XX This sequence represents a novel ligand-binding receptor, zcytor2, which
 XX shares homology with cytokine receptors and was isolated from a human
 XX testis cDNA library. The resulting polypeptide is a receptor for
 XX cytokines (particularly interleukin-13) and is expressed on the surface
 XX of testicular cells, probably being involved in spermatogenesis. It can
 XX be used to detect ligands that promote proliferation and/or
 XX differentiation of such cells in cultures and may also be used to treat
 XX infertility. Antagonists of this receptor may be used to characterise
 XX ligand-receptor interactions and as male-specific contraceptives. By
 XX blocking the action of IL-13, receptor antagonists and ligand-binding
 XX this receptor can also be used to modulate immune function, e.g. in
 XX allergy and asthma, as a diagnostic to determine circulating levels of
 XX ligand and also to isolate and purify ligands. Antibodies can be used to
 XX assay circulating receptor (an abnormal level may be indicative of
 XX disease such as cancer), for labelling cells that express the receptor,
 XX and therapeutically as antagonist.
 XX SQ Sequence 380 AA;

Query Match 98.8%; Score 2078; DB 18; Length 380;
 Best Local Similarity 99.2%; Pred. No. 2.2e-195;
 Matches 377; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLTSTFCTSSDTEIKVNPDPDFEIVDPGLVGLXLOWOPPLSLD 60
 DB 1 mafvclaigclyltltstfctssdteikvnpdpdfeivdpvglvlylqwapplsld 60
 QY 61 HFKECTVEYELKYRNIGSETWTKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkeytveyelkyrnisetwtkititknlhykdgfdlنگkieakihltlpwqctngsevg 120
 QY 121 SSWAETTYTSPQIPETKVQDMDCVYNNQWYLCSWKPKGIGVLLDTNYNLFWYEGLDH 180
 DB 121 sswaettytspqipetkvqdmcdcvynnwqylcswkpgigvllدtnynlfwyegldl 180
 QY 181 ALOCVDYIKADGQNGICRFPPLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNVKPLP 240
 DB 181 alqcvdylkadgqngicrfppleasdykdfyicvngsssenkpirssyftfqlqnvkplp 240
 QY 241 PVYLTFRESSCEIKLKWISPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLTKTNE 300

DB 241 pvyitfressceiklkwgipglpiparcfdyeieireddttlvtatvenetytlktne 300
 QY 301 TRQLCFVVRKSVNLYCSDGDIWSEWSKQWEGEDLSKKTLLRFLWLPFGFILLILVIFVTG 360
 DB 301 trqlcfvvrksvnlcsddgiwsewsdkqwedlskktllrfwlpfgfllilvifvtg 360
 QY 361 LLLRKPNTYPKMPEFFCDT 380
 DB 361 llrrkptntypkmpeffcdt 380
 RESULT 11
 AAW36616
 ID AAW36616 standard; Protein; 372 AA.
 XX AC AAW36616;
 XX DT 30-MAR-1998 (first entry)
 XX DE Celebus macaque zcytor2 protein.
 XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 XX OS Macaque sp.
 XX PH Key Location/Qualifiers
 XX PT Protein 1..372
 XX FT /label= zcytor2
 XX FT /note= "partial protein sequence"
 XX PN WO9733913-A1.
 XX PD 18-SEP-1997.
 XX PF 12-MAR-1997; 97WO-US04043.
 XX PR 13-MAR-1996; 96US-0013345.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 XX PI O'Hara PJ;
 XX DR WPI; 1997-470820/43.
 XX DR N-PSDB; AAT96784.
 XX PS New nucleic acid encoding testis-specific cytokine receptor - useful
 XX PT for identification of ligands or antagonists, potentially for use as
 XX PT male contraceptives or for infertility treatment
 XX FT
 XX PS Example 4; Page 56-57; 79pp; English.
 XX This sequence represents a novel ligand-binding receptor, zcytor2,
 XX which shares homology with cytokine receptors and is isolated from
 XX testis tissue obtained from a Celebus macaque. The resulting polypeptide
 XX is a receptor for cytokines (particularly interleukin-13) and is
 XX expressed on the surface of testicular cells, probably being involved in
 XX spermatogenesis. It can be used to detect ligands promoting proliferation
 XX and/or differentiation of such cells in cultures and may also be used to
 XX treat infertility. Antagonists of this receptor may be used to
 XX characterise ligand-receptor interactions and as male-specific
 XX contraceptives. By blocking the action of IL-13, receptor antagonists and
 XX ligand-binding this receptor can also be used to modulate immune
 XX function, e.g. in allergy and asthma, as a diagnostic to determine
 XX circulating levels of ligand and also to isolate and purify ligands.
 XX Antibodies can be used to assay circulating receptor (an abnormal level
 XX may be indicative of disease such as cancer), for labelling cells that
 XX express the receptor, and therapeutically as antagonist.
 XX SQ Sequence 372 AA;

| Query Match | 88.1% | Score 1853; | DB 18; | Length 372; |
|-----------------------|---|---------------------|-----------|-------------|
| Best Local Similarity | 92.2% | Pred. No. 2.4e-173; | | |
| Matches 343; | Conservative 7; | Mismatches 22; | Indels 0; | Gaps 0; |
| QY 1 | MAFVCLAIGCLYTLTSTTCCTSSDTEIKVNPPODFEIVDPGVLGVLGYLWOPPLSLD | 60 | | |
| DB 1 | MAFVLAIRCCLTCLTSTTGYSTDEIKVNPPODFEIVDPGVLGVLGYLWOPPLSLD | 60 | | |
| QY 61 | HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWCQTNGSEVQ | 120 | | |
| DB 61 | NFKECTVEYELKYRNIGSETWTTIITKNLYKDGFDLNGKIEAKIHTLLPWCQTNGSEVQ | 120 | | |
| QY 121 | SSWAETTYWISPGIPETKQVDMDCVYNNWQYLCSKPKGIGVLLDRTNLYNFYWEGLDH | 180 | | |
| DB 121 | SSWAETTYWISPGIPETKQVDMDCVYNNWQYLCSKPKGIGVLLDRTNLYNFYWEGLDH | 180 | | |
| QY 181 | ALOCVDYIKADGQNIQCRFPYLEASDYKDFICYNGSSSENKPIRSSYTFQLOQIVKPLP | 240 | | |
| DB 181 | ALQCDYIKVQGNIGRFPYLEASDYKDFICYNGSSSENKPIRSSYTFQLOQIVKPLP | 240 | | |
| QY 241 | PVYLTFPRESCEIKLKWISPLGPIPARCFDYETIEIREDDTTLVTAVENETTYTLKTTNE | 300 | | |
| DB 241 | PVCLTCTGESLYEIKLKWISPLGPIPARCFDYETIEIREDDTTLVTAVENETTYTLKTTNE | 300 | | |
| QY 301 | TRQLCFVVRKVNLYCSDDGWSEWSKQCEGEDLSKKTLLRFLWLPFGFTLLILVIFVTG | 360 | | |
| DB 301 | TRQLCFVVRKVNLYCSDDGWSEWSKQCEVEDLKKTLILFILFVIFVTG | 360 | | |
| QY 361 | LLLRKPNTYPRM 372 | | | |
| DB 361 | LLLRKDSYPM 372 | | | |
| RESULT 12 | | | | |
| AAW56261 | AAW56261 standard; Protein; 315 AA. | | | |
| XX | AAW56261; | | | |
| AC | | | | |
| XX | | | | |
| XX | 16-SEP-1998 (first entry) | | | |
| DT | | | | |
| XX | Mature interleukin-13 binding protein. | | | |
| DE | | | | |
| XX | | | | |
| XX | | | | |
| KW | Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis; | | | |
| KW | autoimmune disease; antibody; immunotherapy. | | | |
| XX | | | | |
| OS | Homo sapiens. | | | |
| XX | | | | |
| PN | WO9810638-A1. | | | |
| PD | 19-MAR-1998. | | | |
| XX | | | | |
| XX | 10-SEP-1997; 97WO-AU00591. | | | |
| XX | | | | |
| PR | 27-FEB-1997; 97AU-0005374. | | | |
| PR | 10-SEP-1996; 96AU-0002262. | | | |
| XX | | | | |
| PA | (AMRA-) AMRAD OPERATIONS PTY LTD. | | | |
| XX | | | | |
| PI | Hilton DU, Nicola NA, Simpson RJ, Zhang J; | | | |
| XX | | | | |
| DR | WPI; 1998-207062/18. | | | |
| DR | N-PSDB; AAV22702. | | | |
| XX | | | | |
| PT | New isolated interleukin-13 binding protein - used to develop | | | |
| PT | products for therapy e.g. for allergic conditions such as asthma or | | | |
| PT | for diagnosis or detection | | | |
| XX | | | | |
| PS | Disclosure; Page 55-56; 69pp; English. | | | |
| XX | | | | |
| CC | The IL-13 binding protein and related therapeutic molecules can be used | | | |
| CC | in the antagonism of at least one IL-13 activity. They can be used for | | | |

| | |
|--|---|
| CC | treating IL-13 mediated conditions such as certain allergic conditions |
| CC | such as asthma or to inactivate locally administered IL-13 after IL-13 |
| CC | treatment. The products can also be used as diagnostic agents, e.g. for |
| CC | detecting autoimmune diseases. The antibodies can also be used for |
| CC | immunotherapy and may also be used as a diagnostic tool. |
| XX | |
| SQ | Sequence 315 AA; |
| | |
| | Query Match 83.3%; Score 1753; DB 19; Length 315; |
| | Best Local Similarity 100.0%; Pred. No. 1.2e-163; |
| | Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps |
| QY | 29 EIKVNPQDFEIVDPGYGLYLXIQWPPPSLDHFKECTVEYEKYNIGSEFWKTITN 88 1 eikvnpqdfeiwdpgylylqwpppsldhfkectveyelkynigsetwktitkn 60 |
| Db | |
| QY | 89 LHYKDGFDLNGTEAKTHTLLPWQCTNGSEVSQSSWAETTYWISPOGIPETKYODMDCVYY 148 61 lhykdgfdlnkteakhtllpwqctngsevsqsweettywispgipetkyodmcdcvyy 120 |
| Db | |
| QY | 149 NWOYLCSWRPAGIQLDNTNYNFYWYEGDLHALQCVDYIKADQNIGCRFPYLEASDYK 208 121 nwqyllcswrpkpgivlldntnynfwyegdlhalqcvdykadgnigcrfyleasdyk 180 |
| Db | |
| QY | 209 DFYICVNGSSENKPIRSSYTFQLOINVKLPDPVYLTFTRESSCEIKLKWSPLGPPIPAR 268 181 dfycvngssenkiprissytfqlqnivkplppvyltftressceiklkwsplgpipar 240 |
| Db | |
| QY | 269 CFDEYEIRREDDTLVTATVENETYTLTKTNFTRQLCFVVRSKVNIYCSDDGIWSEMSDK 328 241 cfdeyeirreddtlvtatvenetytltktnetrqlcfvrvskvnlycsddgiwsewsdk 300 |
| Db | |
| QY | 329 QCWEGEDLSKKTLILR 343 301 qcwegedlskktilr 315 |
| Db | |
| RESULT 13 | |
| AAM56260 | |
| ID AAM56260 standard; Protein; 359 AA. | |
| AC AAM56260; | |
| DT DT | |
| DE DE | |
| KW KW | Construct containing mature interleukin-13 binding protein. |
| KW KW | Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis; |
| OS OS | autoimmune disease; antibody; immunotherapy. |
| PN PN | Homo sapiens. |
| PD PD | WO9810638-A1. |
| PX PX | 19-MAR-1998. |
| PX PX | 10-SEP-1997; 97WO-AU00591. |
| PR PR | 27-FEB-1997; 97AU-0005374. |
| PR PR | 10-SEP-1996; 96AU-0002262. |
| PA PA | (AMRA-) AMRAD OPERATIONS PTY LTD. |
| PI PI | Hilton DJ, Nicola NA, Simpson RJ, Zhang J; |
| DR DR | WPI; 1998-207062/18. |
| XX XX | N-PSDB; AAV22701. |
| PT PT | New isolated interleukin-13 binding protein - used to develop |
| PT PT | products for therapy e.g. for allergic conditions such as asthma or |
| XX XX | for diagnosis or detection |

Example 14; Page 52-53; 69pp; English.

PS The IL-13 binding protein and related therapeutic molecules can be used
 XX in the antagonism of at least one IL-13 activity. They can be used for
 CC treating IL-13 mediated conditions such as certain allergic conditions
 CC such as asthma or to inactivate locally administered IL-13 after IL-13
 CC treatment. The products can also be used as diagnostic agents, e.g. for
 CC detecting autoimmune diseases. The antibodies can also be used for
 CC immunotherapy and may also be used as a diagnostic tool.
 XX
 XX Sequence 359 AA;

Query Match 83.3%; Score 1753; DB 19; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.5e-163;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 EIKVNPQDFEIVDPGLYGLYLQWQPLSLDHPKCECTVEYELKYRNIGSETWKTITIKN 88
 DB 45 EIKVNPQDFEIVDPGLYGLYLQWQPLSLDHPKCECTVEYELKYRNIGSETWKTITIKN 104
 QY 89 LHYKDGFDLNGKTEAKTHLLPWQCTNGSEVQSSWAETTTWISPOGIPETKVDMDCVYY 148
 DB 105 LHYKDGFDLNGKTEAKTHLLPWQCTNGSEVQSSWAETTTWISPOGIPETKVDMDCVYY 164
 QY 149 NWQYLLCSWKPGLVLDNINFLYFWEGLDHALQCVDYIKADGONIGCRFPYLEASDYK 208
 DB 165 NWQYLLCSWKPGLVLDNINFLYFWEGLDHALQCVDYIKADGONIGCRFPYLEASDYK 224
 QY 209 DFYICVNGSSNKPIRSYFTFQONIVKPLPPVYLLFTRESSCEIKLWSIPLGPIPAR 268
 DB 225 DFYICVNGSSNKPIRSYFTFQONIVKPLPPVYLLFTRESSCEIKLWSIPLGPIPAR 284
 QY 269 CFDEYEIREDDTFLVATVENETYLTKTNETPQLCFVVRKSNVNIYCSDDGIWSESDK 328
 DB 285 CFDEYEIREDDTFLVATVENETYLTKTNETPQLCFVVRKSNVNIYCSDDGIWSESDK 344
 QY 329 QCWEGEDLSKKTLLR 343
 DB 345 QCWEGEDLSKKTLLR 359

RESULT 14
 AAW35294
 ID AAW35294 standard; Protein; 383 AA.
 XX AAW35294;
 AC AAW35294;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Murine IL-13 binding chain of the IL-13 receptor.
 XX
 KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= signal_sequence
 FT /note= "putative"
 FT 22..383
 FT Protein /label= mature_protein
 FT 22..334
 FT Domain /label= extracellular_domain
 FT 335..356
 FT Domain /label= transmembrane_domain
 FT 357..383
 FT Domain /label= intracellular_domain
 XX
 XX W09731946-A1.
 XX

PD 04-SEP-1997.
 XX
 XX 28-FEB-1997; 97WO-US03124.
 XX
 XX 01-MAR-1996; 96US-0609572.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;
 PI
 DR WPI; 1997-448632/41.
 DR N-PSDB; AAT75213.
 XX
 PT New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis
 XX
 PS Claim 11; Pages 30-31; 49pp; English.
 XX
 CC The present sequence represents the murine interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied.
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.
 XX
 SQ Sequence 383 AA;

Query Match 56.8%; Score 1194.5; DB 18; Length 383;
 Best Local Similarity 58.9%; Pred. No. 9.1e-109;
 Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
 QY 1 MAFVCLAIGLTYFLJSTFTGCTSSSDTEIKVNPQDFEIVDPGLYGLYLQWQPLSLD 60
 DB 1 marv--hircicfillctitgys----leikvnpqgqfelfdpilgylgikwppvvie 54
 QY 61 HFRECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKTEAKTHLLPWQCTNGSEVQ 120
 DB 55 kfgctleyelkyrnvdswkktitrlniykdgfdlنگkiegkirtlhsehctngsevg 114
 QY 121 SSAETTYWISPOGIPETKVDMDCVYNNWQYLCSWKPGLVLDNINFLYFWEGLDH 180
 DB 115 spweasysgidsgeletkigdmkciyynwgylvcswkpgktvysdntymffwyegldh 174
 QY 181 ALQCVDIKADGONIGCRFPYLEASDYKDYICVNGSSNKPIRSYFTFQONIVKPLP 240
 DB 175 alqcadylqhdnkvngcklnldssdykdficvngsskleiprissyvtfqlgnvkplp 234
 QY 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYETIREDDTTLVATVENETYLTKTNE 300
 DB 235 pefihisvensidirmkswstpggipiprcytyelvireddiswesatdkndmklkrane 294
 QY 301 TROLCFVVRKSNVNIYCSDDGIWSESDKQCWEGEDLSKKTLLRFLWLPFGFILLIVFTG 360
 DB 295 sedlcffvrckvnlcaddglwsewseecewgytgdpskii-fivpvcffiflilllc 353
 QY 361 LLRLKPNTPYKPM 372
 DB 354 livekeepeptl 365

RESULT 15

AA95295
 ID AA95295 standard; Protein; 383 AA.
 AC AA95295;
 XX 12-SEP-2000 (first entry)
 DT
 XX IL-13 binding chain of mouse IL-13 receptor.
 DE
 XX Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
 KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
 KW immune complex disease; lupus; nephritis; thyroiditis;
 KW Grave's disease; inflammatory; infection; therapy; antiallergic;
 KW antiinflammatory; antiasthmatic; vaccine.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..383
 FT /note= "mature protein"
 FT Domain 22..334
 FT /note= "extracellular domain; a polypeptide
 FT comprising amino acids 22-334 is
 FT specifically claimed in Claim 11(b)"
 FT Domain 335..356
 FT /note= "transmembrane domain"
 FT Domain 357..383
 FT /note= "intracellular domain; a polypeptide
 FT comprising amino acids 257-383 is
 FT specifically claimed in Claim 11(c)"
 XX
 PN WO200036103-A1.
 XX
 XX 22-JUN-2000.
 XX
 XX 13-DEC-1999; 99WO-US29493.
 XX
 XX 14-DEC-1998; 98US-0211335.
 XX
 XX (GENY) GENETICS INST INC.
 XX (UMJO) UNIV JOHNS HOPKINS.
 XX
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 FI Wills-Karp M;
 XX
 XX WPI; 2000-431587/37.
 XX N-PSDB; AAA27911.
 XX
 XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
 PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
 PT asthma, Grave's disease and inflammatory conditions of the lung -
 XX
 XX Claim 11(a); Page 50-51; 60pp; English.
 XX
 XX The present sequence is that of the interleukin-13-binding chain
 CC (IL-13bc) of the murine IL-13 receptor, as deduced from an isolated
 CC C3H/HeJ mouse thymus cDNA clone (see AAA27911). IL-13bc is a member
 CC of the haematopoietin receptor family that acts as a mediator of
 CC IL-13. The invention provides methods for the recombinant
 CC production of IL-13bc polypeptides, including claimed full-length
 CC IL-13bc, its extracellular domain, and its intracellular domain.
 CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
 CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
 CC of IL-13 and its receptor) can be used to treat conditions in
 CC which IL-13 is implicated, particularly IgE-mediated conditions and
 CC diseases including atopy, allergy, asthma, immune complex diseases
 CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
 CC thyroiditis and Grave's disease), lung inflammation,
 CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
 CC activation, IL-13bc proteins can also be used to enhance macrophage

CC activation, e.g. in vaccination, treatment of mycobacterial or
 CC intracellular organisms or parasite infections. IL-13bc proteins
 CC may also be used to potentiate the effects of IL-13 in vitro and
 CC in vivo, as diagnostic agents, and to screen for agents capable of
 CC binding to IL-13bc or IL-13 receptor, or which interfere with the
 CC binding of IL-13 to its receptor.
 XX
 XX Sequence 383 AA:

Query Match 56.88; Score 1194.5; DB 21; Length 383;
 Best Local Similarity 58.9%; Pred. No. 9.1e-109;
 Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
 QY 1 MAFVCLALGCLYELFLISTFTGCTSSSDTEIKVNPQDFEIVDPGVLGVLQWPPPLSLD 60
 Db 1 mafv--hircfcilictitgys----leiknpqdfelidpallgylqlwppvvie 54
 QY 61 HFRECTVEYELKYRNIGSETWTKTITITKNLHYKDGFDLKNKIEAKIHTLLPMQCTNGSEVQ 120
 Db 55 kfgctleyelkyrnvdssdsktittlnliykdgfdlnkgiegkirthlsehtngsevg 114
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYVEGLDH 180
 Db 115 spwieasygisdegslctkiqdmkciyynwqylvcskpgktytsdntymffwyegldh 174
 QY 181 ALQCVDYIKADGQNGICRFPVLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
 Db 175 alqcadyiqhdekngvcklsnldssdykdficvngsklepirssytcvfglnlvkplp 234
 QY 241 PVLTFTRRESCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTVATVENETYTLTKTTNE 300
 Db 235 pefihisvensidirmkwstpggpiprcyeyeiaveddiswesatdkndmkikrrane 294
 QY 301 TRQLCFVVRKVNIIYCSDDGIWSEWSKQCWEGEDLSKKTLRLFWLPEGFILILVIFVTG 360
 Db 295 sedicffvrckvniycaddgiwsewseeecwegytpgdsksii-fivpvcilffillilc 353
 QY 361 LLRLKPNITYPKM 372
 Db 354 livekepeptci 365

Search completed: September 1, 2001, 19:07:03
 Job time: 70 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:05:53 ; Search time 43.66 Seconds
(without alignments)
662.994 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: -2104

Sequence: 1 MAFVCLAIGCLYFLISTTF.....LLLRKPNTPYKMPIEFFCDT 380

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 311.5 | 14.8 | 420 | 2 S21052 | interleukin-5 rece |
| 2 | 292 | 13.9 | 335 | 2 A40267 | interleukin-5 rece |
| 3 | 263 | 12.5 | 831 | 2 J01655 | prolactin receptor |
| 4 | 247 | 11.7 | 415 | 2 S12357 | interleukin-5 rece |
| 5 | 220 | 10.5 | 369 | 2 A42565 | prolactin receptor |
| 6 | 216.5 | 10.3 | 830 | 2 I50455 | interleukin-2 rece |
| 7 | 212.5 | 10.1 | 369 | 2 I49280 | interleukin-2 rece |
| 8 | 208 | 9.9 | 373 | 2 A55718 | interleukin-3 rece |
| 9 | 195 | 9.3 | 878 | 1 A40091 | cytokine receptor |
| 10 | 180.5 | 8.6 | 897 | 1 A39255 | interleukin-3 rece |
| 11 | 178 | 8.5 | 896 | 2 I56563 | cytokine receptor |
| 12 | 173.5 | 8.2 | 896 | 1 A35762 | prolactin receptor |
| 13 | 165 | 7.8 | 310 | 2 A29884 | prolactin receptor |
| 14 | 165 | 7.8 | 412 | 2 A41070 | prolactin receptor |
| 15 | 165 | 7.8 | 581 | 2 I45971 | prolactin receptor |
| 16 | 165 | 7.8 | 610 | 2 A34631 | prolactin receptor |
| 17 | 165 | 7.8 | 610 | 2 A36116 | prolactin receptor |
| 18 | 160.5 | 7.6 | 303 | 2 I77524 | prolactin receptor |
| 19 | 159 | 7.6 | 292 | 2 I77525 | prolactin receptor |
| 20 | 159 | 7.6 | 608 | 2 I53269 | prolactin receptor |
| 21 | 151 | 7.2 | 622 | 2 A40144 | prolactin receptor |
| 22 | 150.5 | 7.2 | 917 | 2 I49699 | glycoprotein 130 - |
| 23 | 149 | 7.1 | 616 | 2 A30304 | prolactin receptor |
| 24 | 142.5 | 6.8 | 400 | 2 S06945 | granulocyte-macrop |
| 25 | 138 | 6.6 | 378 | 2 A40266 | interleukin-3 rece |
| 26 | 134.5 | 6.4 | 1097 | 2 S17368 | leukemia inhibitor |
| 27 | 133.5 | 6.3 | 333 | 2 S13684 | granulocyte-macrop |
| 28 | 133.5 | 6.3 | 378 | 2 S50040 | granulocyte-macrop |
| 29 | 131.5 | 6.2 | 630 | 2 I51086 | prolactin receptor |

ALIGNMENTS

RESULT 1

S21052

interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C:Accession: S21052; S21053; A46175; S78106; S78107
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815
A:Accession: S21052

A:Molecule type: DNA

A:Residues: 1-420 <MUR>

A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A:Experimental source: clone lambda h5R.12

A:Accession: S21050

A:Molecule type: DNA

A:Residues: 1-395, 'I' <MU2>

A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A:Experimental source: clone lambda h5R.27

A:Accession: S21053

A:Molecule type: mRNA

A:Residues: 1-332, 'K' <MU3>

A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A:Experimental source: clone lambda h5R.25

R:Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992

A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum
A:Reference number: A46175; MUID:92357767

A:Accession: A46175

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 333-420 <TAV>

A:Experimental source: HL-60 cells and eosinophils

A:Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)

R:Murata, Y.

submitted to the EMBL Data Library, July 1991

A:Reference number: S78106

A:Accession: S78106

A:Molecule type: DNA

A:Residues: 1-128, 'I', 130-395, 'I' <MUW>

A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

R:Murata, Y.

submitted to the EMBL Data Library, September 1991

A:Reference number: S78107

A:Accession: S78107

A:Molecule type: mRNA

A:Residues: 1-128, 'I', 130-332, 'K' <MU4>

A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

F:345-365/Domain: transmembrane #status predicted <TM>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.8%; Score 311.5; DB 2; Length 420;
Best Local Similarity 26.9%; Pred. No. 3.1e-17;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDFEIVDPCYGLVLYLQWPPPLSLDHFKECTVEYELKYNIGSETWKTIIT 86
DB 25 DEKISLLPVPVFTIKVTG-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPKEDDIYETRI 82
QY 87 KNLHYKDGFLNKGTEAKIHTLLPQCTNGSEVOSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSASVRILO---NDHSILLASSWASAEHL-APGSPGTSVNLCT 135
QY 147 -----YNNQYLL-CSWKGIGVLLDTNLFY----WYEGDLHALQCVDIKAD 191
DB 136 TTTTNDYNSRLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLQNIKPLPPVVLFT 248
DB 190 LGRNIACWFPRTFILSKGRDMLVNGSSSKHSAIRPDFQALFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVTATVENETTYLTNTNETRQLCFVV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIHNRNGYLOIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWSKOCWGEDLSKTLIRFVLPFGFIIL-----VIFVTVGLL 362
DB 309 RAAVSSMCREAGLWSEWS-QPIYGVNDEHKP--LREW---FVIVIMATICFILLILSLI 361
QY 363 LRKPNTYPMKP 374
DB 362 CKICHLWIKLFP 373

RESULT 2
A40267
Interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuppens, T.; Van der Heyden, J.; Fiers, W.; Pl
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-spec
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 13.9%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 8.2e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPQDFEIVDPCYGLVLYLQWPPPLSLDHFKECTVEYELKYNIGSETWKTIIT 86
DB 25 DEKISLLPVPVFTIKVTG-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPKEDDIYETRI 82
QY 87 KNLHYKDGFLNKGTEAKIHTLLPQCTNGSEVOSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSASVRILO---NDHSILLASSWASAEHL-APGSPGTSVNLCT 135
QY 147 -----YNNQYLL-CSWKGIGVLLDTNLFY----WYEGDLHALQCVDIKAD 191
DB 136 TTTTNDYNSRLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLQNIKPLPPVVLFT 248
DB 190 LGRNIACWFPRTFILSKGRDMLVNGSSSKHSAIRPDFQALFALHAIQINPLNVTAEI 249

DB 190 LGRNIACWFPRTFILSKGRDMLVNGSSSKHSAIRPDFQALFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVTATVENETTYLTNTNETRQLCFVV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIHNRNGYLOIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWS 326
DB 309 RAAVSSMCREAGLWSEWS 326
RESULT 3
JQ1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: kidney
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 12.5%; Score 263; DB 2; Length 831;
Best Local Similarity 26.4%; Pred. No. 5.3e-13;
Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

QY 18 TTFGCTSSSTETKVN---PPQDFE---IVDPG-----YLGYYLQWPPPLSL 59
DB 97 TTFNTITVATNEIGSSSDPQYVDVTSIVQSPVNLTLTKRSANIMYLWAKWSPPLA 156
QY 60 DHFKECTVEYELKYNIGSETWKTIITKNLHYKDGFLNKGTEAKIHTLLPQCTNGSEV 119
DB 157 DASSNHLHYELRLKPEKEWEETI---SVGVQTOCKINR-LNAGMYVYVQVRCITLDPGE 212
QY 120 QSSWAETTYWISPOG-IPETKVQDMDCVYNNQYLLCSWKGIGVLLDTNLYFYWEGL 178
DB 213 WSEWSSERHILIPSGQSPPEKPTTIKCRSPEKETFTCWKPKGLDGGHPTNVTLLYSKEGE 272
QY 179 DHALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLQNIKVP 238
DB 273 EQVEYCPDY-RTAGPN-SCYFDKKHTSFWTIYNITVTRATNEMGSSSDPHYVDVTVIQP 330
QY 239 LPPVLLFTRESSCEIK-----LKWS-IPLGPIPARCFDYEIETIR---EDDTTLVTATVEN 290
DB 331 DPPVNVTELEKPKINRPPVLLVWSPPLADVRSGWLTLEYELKPEEGEWEETIFVQ 390
QY 291 ET-YTLKTTNETRQLCFVVRSKVNIYCSDD--GIWSEWSKQWCE-GEDLSKTLIRLFWL 346
DB 391 QTOYKMFSLNPGKKYI-----IQIHCCKPDHGSWSEWSSENYIQIPNDFRVKDMI-VWI 443
QY 347 PFGFI--LILVIFVTGLLRLKPNTPYPMKP 374
DB 444 VLGVLSLLICLIMSWTMLKGYRMITMLP 473

RESULT 4
S12357
Interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)

R;Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.
Hum. Mol. Genet. 2, 1099-1104, 1993
A;Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11
A;Reference number: I54332; MUID:94004847
A;Accession: I54332
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-369 <RE2>
A;Cross-references: GB:I19546; NID:g349631; PIDN:AAC37524.1; PID:g349632
C;Genetics:
A;Gene: GDB:IL2RG; SCIDX1: IMD4
A;Cross-references: GDB:I34807; OMIM:308380
A;Map position: Xq13.1-Qx13.1
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A;Note: defects are associated with an x-linked form of severe combined immunodeficiency
C;Superfamily: Interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunodeficiency

Query Match 10.5%; Score 220; DB 2; Length 369;
Best Local Similarity 25.5%; Pred. No. 4.9e-10;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

QY 97 LNKGIEAKIHTLPLWQCTNGSE-VOSSWAETTWISQGPETKVDMDCVYNWVLLC 155
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 19 LGVGLNTLTIT-----PNGNEPTADFTTMTPTDSLVSSTLPLPEVQCFFVNVEYMC 72
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 156 SW-----KPGIGVLLDTNTLFWYEGLDH--ALQCVDYIKADQNIGCRFPYLEASDY 207
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 73 TWNSSSPQP-----TNLTWHYKNSDNCKVKOKSHLYFSEEITSGCOLQKKEIHLY 125
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 208 KDFYICVGVSSGNKPRISSYFTFQLQNVAPLPVPVYTFTRESSCEIKLWSIPLGPIPA 267
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 126 QTFVVOQLQDPRE--PRQAOTMLKLQNLVIPWAPENLTHLKSESQLELNWN---NRFLN 180
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 268 RCFDYEIERED-DTLVLVTATVE-NETYTLKTNETRQLCFVVRSKVNIYCSDDGIIWSEW 325
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 181 HCLEHLVQYRTDWDHSWTEQSVDYRRHKFSPLPSVDGQKRYYTRFRSRENPLCGSAQHWEW 240
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 326 SDKOCWGEDLSKTKLLRFWLPGCFILLIVFYTG 360
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 241 SHPIHW-GSNATSKEN-----PFLFAEAVVISVG 268
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
I50455
prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C;Accession: I50455
R;Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor
A;Reference number: I50455; MUID:94283267
A;Accession: I50455
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-830 <CHE>
A;Cross-references: EMBL:U07694; NID:g456381; PIDN:AAA20646.1; PID:g456382
C;Superfamily: cytokine receptor homology
F;36-220/Domain: cytokine receptor homology <CRSL>
F;240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.3%; Score 216.5; DB 2; Length 830;
Best Local Similarity 24.4%; Pred. No. 2.6e-09;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

QY 18 TFGCTSSSDTEKLVNPQDFEIVDCPYLG-----YLYLOW 53
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 97 TTNTITVMANNEIGSNS-----DPQIVDVTSIQDPAPVNLSETKTSASTYLLAKW 150
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 54 QPPLSLDHFKECTV-EYELKYRNIGSETKTIITKNLHYKDGFOLNKGIKAHIHTLLPWQ 112

Db 151 SPPLADVTNSHVYRRLRLKPEKEWETV--SVGQYQYKVNRLQAGVYVYQVR 206
 QY 113 CTNGSEVOSSWAETWYISPOG-IPETKQVDMDCVYNNQYLLCSWPGICGVLDITNVL 171
 Db 207 CVLDIGENSESSERHIIPNGESPPKPTTIKRSPEKETFTCWKPGSDGGHPTNYTL 266
 QY 172 FWVEGLDHALQVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQ 231
 Db 267 LYSKEGERVECDPY-KTAGPN-SCYFDKHTSFWIYNTVATNEIGNSVDPLVYD 324
 QY 232 LONIVKPLPPVYLFTRESSCEIK----LKWS-IPLGPIPA--RCFDYIEIREDDTTLV 284
 Db 325 VYIIVQDTPPVNVITLKKTKVNRKPYLVLTWSPPLADVRSGWLTLDYELRLKPEEA--- 381
 QY 285 TATVENETYLKTNETRQICFVV----RSKNVICYSD--GINSWS-DKQCEGEDLS 337
 Db 382 -----EWEETIFVQOQTHYKMFSLNPGKKYIVQIHCRPDHRSWSWSLEKYLIQPTDFR 436
 QY 338 KKTLLRFLWLPFGFILLIVFV 358
 Db 437 IKDMV-VWIIVGVLSLICLV 456

RESULT 7
 149280
 Interleukin-2 receptor gamma chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: I49280; A47514; JN0592; JN0775; S37582; 153398
 R:Cao, X.; Kozak, C.A.; Liu, Y.
 A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) g
 A:Reference number: A47514; MUID:93391374
 A:Accession: I49280
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <CAO>
 A:Cross-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350
 A:Accession: A47514
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-369 <RE2>
 A:Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
 Biochem. Biophys. Res. Commun. 193, 356-363, 1993
 A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of funct
 A:Reference number: JN0592; MUID:93277575
 A:Accession: JN0592
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-369 <KUM>
 A:Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
 R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
 Gene 130, 303-304, 1993
 A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
 A:Reference number: JN0775; MUID:93366191
 A:Accession: JN0775
 A:Molecule type: mRNA
 A:Residues: 1-369 <KOB>
 A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
 R:Chiu, R.K.; Dougherty, G.J.
 submitted to the EMBL Data Library, October 1993
 A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
 A:Reference number: S37582
 A:Accession: S37582
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
 A:Cross-references: EMBL:X75337
 R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
 Eur. J. Immunol. 24, 3014-3018, 1994
 A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal l

A:Reference number: I53398; MUID:95104285
 A:Accession: I53398
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <RES>
 A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
 C:Genetics:
 A:Gene: IL-2Rgamma
 A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
 A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet
 eptors.
 C:Function:
 A:Description: receptor for interleukin-2
 A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
 F;256-284/Domain: transmembrane #status predicted <TM>
 F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 10.1%; Score 212.5; DB 2; Length 369;
 Best Local Similarity 26.9%; Pred. No. 1.9e-09;
 Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKQVDMDCVYNNQYLLCSW----KPGIGVLDITNVLFWYEGLDHAL--OCVDYIK 189
 Db 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPPQA-----TNLTLYRYKVSNDNTFQCSHYLF 107
 QY 190 ADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNIYKPLPPVYLITRE 249
 Db 108 SKEITSGCQIKEDILYQYFVVQL--QDPQKQRAVQKLNQLNVLPRAPENLTLSNL 165
 QY 250 SSCBIKLKWSIPGLPIPARCFDYIEIREDD--DTTLVTATVENE--TYILKTNETNRQICFV 307
 Db 166 SESQLELRWK--SRHIKERCILQYLVQYRSNDRSMTIELIVNHPEFSLPSVDELKRYTER 223
 QY 308 VRSKNVICYSDDGWTSWSKQCEG-----EDLSKKTLLRFLWLPFGF--ILILVIFVTGL 361
 Db 224 VRSRYNICGSSQWKSQPVHWSHTVENPSLFALEAVLIPVGTMLITLIFVYCW 283
 QY 362 LLRKPNTPY 370
 Db 284 LERMPPIPP 292

RESULT 8
 A5718
 Interleukin-2 receptor gamma chain precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
 C:Accession: A5718
 R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
 Genomics 23, 69-74, 1994
 A:Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combi
 A:Reference number: A5718; MUID:95130114
 A:Accession: A5718
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-373 <HEN>
 A:Cross-references: GB:U04361; NID:g517411; PIDN:AAC48403.1; PID:g517412
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication

Query Match 9.9%; Score 208; DB 2; Length 373;
 Best Local Similarity 26.0%; Pred. No. 4.5e-09;
 Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

QY 115 NGSE-----VQSSWAETWYISPOGIPETKQVDMDCVYNNQYLLCSW-----RPGI 161
 Db 31 NGNEDITPDPFFLTATPSET---LSVSLPLPEVQ---CFVFNVEYMNCTWNSSEPPR-- 82

Db 358 YSLHWETQKIP--KYIDHTFOVQKKKSSWKDSTENLRVNSMDLPQLEPDTSYCAR 414
 QY 308 VRSK-VNIYCSDDGIWSEWSDKQCEWEGEDLSKTLRLFWLPFGFILLIVLFTVTLGLL 363
 Db 415 VRVKPISDY---DGINSEWSNEYTWT-TDVMPTL---WI-----VLILVFLIFLTLL 460

RESULT 10
 A39255
 cytokine receptor common beta chain precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
 C:Accession: A39255
 R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
 Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
 A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-
 A:Reference number: A39255; MUID:91088571
 A:Accession: A39255
 A:Molecule type: mRNA
 A:Residues: 1-897 <HAY>
 A:CROSS-references: GB:M38275
 C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
 C:Genetics:
 A:Gene: GDB:CSF2RB
 A:CROSS-references: GDB:126838; OMIM:138981
 A:Map position: 22q13.1-22q13.1
 C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
 C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane prote
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-897/Product: cytokine receptor common beta chain #status predicted <MAT>
 F:17-443/Domain: extracellular #status predicted <EXT>
 F:35-232/Domain: cytokine receptor homology <CRS1>
 F:250-431/Domain: cytokine receptor homology <CRS2>
 F:444-460/Domain: transmembrane #status predicted <TM>
 F:461-897/Domain: intracellular #status predicted <INT>

Query Match 8.6%; Score 180.5; DB 1; Length 897;
 Best Local Similarity 22.6%; Pred. No. 2.1e-06;
 Matches 90; Conservative 58; Mismatches 146; Indels 105; Gaps 21;

QY 32 VNPQDFEIVDPGLGY-----LYLOWQPP-----LSLQHP----- 62
 Db 97 VIPCQSFVTDVDFSPQDRPLGTRLTVTLTQHVQPEPRDLQISTDQDHFLLTWSVAL 156
 QY 63 -----KECTVEYELKYNIGSETWK--TIITKLNLYKDGFLNKGIE-----A 103
 Db 157 GSPQSHWLSPCDLEFEVVKRL-QDSWEDAILLSNTS-----QATLGPEHLMSPSYVA 210
 QY 104 KIHT-LLPMOCTNGSEVOSSWAETTYIWSQIGIPETKVQDMDCVYINWQYLLCSWKPGIG 162
 Db 211 RVRTLRAPGSRSLGR--PSKSWPEVCWDSOPG-DEAQPNLECFCDGAALVSCSWEVKRE 267
 QY 163 VLLDTNVLNFWBGLDHALQVDYIKADGNQIG-----CRPPYLEASDYKDFYICVN 215
 Db 268 VASVSFGLFKPSPDAGEECSPVLR---EGLSLTRHHCQIPVDPDPATHQGYIVSVQ 324
 QY 216 GSSENKPIRSYFTFQNLQIVKPLPPVYLTFRESSCEIKLWKSIPGLPIPARCFDYEIE 275
 Db 325 PRRAEKHIKSSV-----NI-QMAPPSLNVTKDGD-SYSLRWETMKMRVEIHDTTEIQ 375
 QY 276 IREDDTTLVTAT-VENETYILKITN-----ETQLCFV-VRSKNVYICSDDGTWSE 324
 Db 376 YRKD-----TATWKDSKTETLQNAHSMALPALEPSTRYKARVVRTSGY---NGIWE 427
 QY 325 WSKQCEWEDLSKTLRLFWLPFGFILLIVFTVTLGLL 363
 Db 428 WSEARSDTESV-----LPMWVLIIVIFLTAVL 457

RESULT 11
 156563

interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C:Genetics:
A:Gene: rIL-3Rbeta
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>
F:23-441/Domain: extracellular #status predicted <EXT>
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-434/Domain: cytokine receptor homology <CRS2>
F:442-463/Domain: transmembrane #status predicted <TMM>
F:464-896/Domain: intracellular #status predicted <INT>

Query Match 8.5%; Score 178; DB 2; Length 896;
Best Local Similarity 21.4%; Pred. No. 3.3e-06;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLAIGCL--YT-FLISTTFCGTSSTDEIKVN-----PPQDFEIVDPGILGYL 49
Db 94 CVPRRCVLPYTFQSVSKEDYISLQPDRLSLHLVPLAQHVQPPPKDISPSG--DHF 151
QY 50 YLQWQPL---SLDHFKECTVEYELKYNIGSETWTKIITKNLHYKDGFDLNGKIEAKIH 106
Db 152 LLKWSVSLGDAQVLLSQDKQFEVAYKQL-QDSWED-----TCNLWVTLEPK 203
QY 107 TLLP-----WQCTNGSEVQ---SSWAETTYWISPOGIPETKVDMDCVYNNWQYLL 154
Db 204 LFLNSIYAVRAQLAPGSLGRSGWSEVHWDSPTE-DKARPQNLQCFDGIQSLN 262
QY 155 CSWPGIGVLLDTNLYNFWYEGDLHALQCVDIKADGQNGICRFPYLEASDYKDFYICV 214
Db 263 CSWEWTKVTDVSFGLFYSSPKAGEKCSPPVKE-----LQASRYTRYHCSL 311
QY 215 NGSENPIRSYTFQLO-----NIVKPLPP-VYLTFTRESSCEIKLWKSPI 262
Db 312 NVSD---PAASHQYTSVSKRLEQKGFIEFNHIQMNPTLNLTKNRDS---YSLHWETQK 365
QY 263 GPIPARCFDYEIR-----EDDTTLVATVENETTLKTNTRQLCFVRSKVNICY 316
Db 366 MSYPIQHAFOVQYKKLDRWEDSKT-----ENLHAHSMDLQLEPQTSYCARVRVKTI 421
QY 317 SDDGIWSEWSKQCEGEDLSKTKLLRFLWLPFGFILIVFVTGLLL 363
Db 422 EYKGLWSEWSNECTWT-TDWMVPTL---WI-----VLILVFLILTL 460

RESULT 12
A35782
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Aral, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein
A:Reference number: A35782; MUID:90319131
A:Accession: A35782
A:Molecule type: mRNA
A:Residues: 1-896 <GOR>
A:Cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>

Query Match 8.2%; Score 173.5; DB 1; Length 896;
Best Local Similarity 20.7%; Pred. No. 7.5e-06;
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

QY 5 CLAIGCLYTFLLISTFTFCTS-----SSDTEIK-----VNPQDFEIVDPGILGY 48
Db 94 CVPRRCVPIPY---TRFSITNEDYISFRPDSDLGIQLVPLAQNVQPPPLPKNVSSSEDR 150
QY 49 LYLQWQPL---SLDHFKECTVEYELKYNIGSETWTKIITKN-----LHYKDGFDLNGK 100
Db 151 FLLEWSVSLGDAQVSWLSKSDIEFEVAYKRL-QDSWEDAYSHTSKFQVNPPEKFLPLNS 209
QY 101 IEA-KIHT-LLPWOCTNGSEVQSSWAETTYWISPOGIPETKVDMDCVYNNWQYLLCSWK 158
Db 210 IYAPRVTRILYPCSSLSGR--PSRWSPEAHWDSPG-DKAQPQNLQCFDGIQSLHCSWE 266
QY 159 PGIGVLLDTNLYNFWYEGDLHALQCVDIK-ADGQNI-----GCRFPYLEASDYKDFYIC 213
Db 267 VWTQTGVSFGLFYRPSVPAPEKCSPPVVKPGASVYTRYHCSLPVPEPSAHSQYTVS 326
QY 214 VNGSENKPIRSYTFQLOINIVKPLPPVYLTFTRESSCEIKLWKSPIGLIPARCFDYE 273
Db 327 V-----KHLEQKGFIMSYNHIQMEPTLNLTKNRDS---YSLHWETQKWAYSFIET 377
QY 274 IEIREDDTLVATVEN--ETYTLTKTNTRQLCFVRSKVNICYSDGDIWSEWSKQCV 331
Db 378 VOYKKKSDSWEDSKTENLDRAHSMDLQLEPDTSYCARVRVKPISNYDGIWSEWSEYTW 437
QY 332 EGEDLSKTKLLRFLWLPFGFILIVFVTGLLL 363
Db 438 K-TDWMVPTL---WI-----VLILVFLILTL 461

RESULT 13
A29884
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C:Accession: A29884
R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ederly, M.; Shirota, M.; Banvi
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth
A:Reference number: A29884; MUID:88165059
A:Accession: A29884
A:Molecule type: mRNA
A:Residues: 1-310 <BOU>
A:Cross-references: GB:M19304; NID:g206364; PIDN:AAA1937.1; PID:g206365
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-310/Product: prolactin receptor #status predicted <MAT>
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 7.8%; Score 165; DB 2; Length 310;
Best Local Similarity 28.5%; Pred. No. 9.2e-06;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

QY 131 SPQGIPEKTVQDMDCVYNNWQYLLCSWKPGIGVLLDTNLYNFWYEGDLHALQCVDIKA 190
Db 21 SPQKPEIH---KCRSPDKETETFCWNPCTDGLPTNYSILTSYKEGKTYECPDY-KT 75
QY 191 DQGNICRFPYLEASDYKDFYICVN-----GSSENKPIRSYTFQLOINIVKPLPPVILT 245
Db 76 SGPN-SCFFSKQYTSIKWIIITVNATNQMGSSSDPL-----YVDVTYIVEPEPPRNL 129

QY 246 F-----TRESSECEIKLWSIP-LGPIPARCDDYEIEIEDDTTLVATVENEYTYTLKTTNE 300
Db 130 LEVKOLDKKTYLKVKKWSPPTITDVKGWETMEYER-----LKPEEAEEWEIHFTGH 182
QY 301 TROL-----CFVVRSKVNIYCSDDGIWSEWSDKOCWE 332
Db 183 QTQFKVFDLYPGQKYLVTQTRCK---PDHGYWSRWQSQSSVE 220

RESULT 14
A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000
C:Accession: A41070; I53417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin receptor
A:Reference number: A41070; MUID:92041834
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390
R:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
A:Reference number: I55417; MUID:95014432
A:Accession: I55417
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964
A:Experimental source: Nb2-11C cell line
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:31-216/domain: cytokine receptor homology <CRS>

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Query Match          7.8%; Score 165; DB 2; Length 412;
Best Local Similarity 28.5%; Pred. No. 1.3e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

QY   131 SPQGIPETKVDMDCVYNWQYLCSNKPGLGVLLDTNNLFWYVEGLDHALQCVDYIKA 190
      ||| ||| : : | | | | | | | | | | : | | |
Db    21 SPPGKPEIH-----KCRSPDKFTFCWNPNPGTDGGLPNTSYLSYSKEGEKTIVCEPDY-KT 75

QY   191 DGONIGRCFPYLEASDYKFICVN----GSSENKPIRSRYFFTLQLONIVKPLPVPVLT 245
      ||| ||| : : | | | | | | | | | | : | | |
Db    76 SGPN-SGFFSKOYTISWKIYYITNATNQMGSSSDPL-----YDVTFYIVEPEPRNLTT 129

QY   246 F---TRESCIEIKLWSIP-LGPAPRCFDFYEIRDDTTLTVATVENETYTLTKTNE 300
      :: :|||:: :|||:: :|||:: :|||:: :|||:: :|||:: :|||:: :|||:: :|||
Db    130 LEVKOLDKKTYLVNWKNSPPITDVKTCGWTFMEYR-----LKPEAEWEHFHTGH 182

QY   301 TRQL-----CFVVRKSKNVIYCSDDGIIWSEWDKOCWE 332
      - :|::|:: :|||:: :|||:: :|||:: :|||:: :|||:: :|||:: :|||
Db    183 QTQFKVFDPYGKYVLGTQCK--PDHGYSRWQSQESSVE 220


RESULT 15
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A>Title: Molecular cloning of the bovine prolactin receptor and distribution of
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
```


QY 01 HFRECVIEELKRIYNLGSETWYIIIFNLHYKDGFDLNNKGIEAKIHTILFLFPWQCTNGSEVQ 11

db 55 KFKGCRLEVEELKYRNVDSWSKTIITRNLYKDGFDLNNKGIEGKIHTILSHCTNGSEVO 112


```

Db 362 CKICHLWIKLFP 373
      : : : | : |
RESULT 4
Q920K4 PRELIMINARY; PRT; 415 AA.
AC Q920K4
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.
GN GFL-5RA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Norris T.E.;
RT "Cloning and Characterization of the Guinea Pig Interleukin-5 receptor
alpha cDNA.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U55215; RAD0361.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 1.
DR DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA.
SQ SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match 14.2%; Score 298.5; DB 11; Length 415;
Best Local Similarity 26.5%; Pred. No. 1.1e-18;
Matches 103; Conservative 67; Mismatches 172; Indels 47; Gaps 19;

QY 6 LAICGLYFLSTVFGTSSDTEIKVNPQDFEIVDPGLYLYLQWQPLSLDHPKEC 65
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 7 ILGAIETLQDTL-----PDKRFLPLPPINFITKVTG-LAQVVLQWEPNQGQ-KNV 58
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 66 TVEYELRYNIGSETWTKITIKNHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVOSSWAE 125
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 59 NLNVHVKINTPQEDYE---TRNTQSKCETLHQGVASVETIL-WH--GHSLLASSWVS 112
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 126 TTYWISPOGIPETKVQDMDCV-----YNNWQ----YLLCSWRKPGIGVLLDTNLYFY- 173
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 113 AEH-KAPPGSPGTSIVNLCTTNTAASNYTNLKSVEYSLHCTWLAGDKADPEDTQYFLYR 171
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 174 ---WYEGLDHALQCVDIKAD-GONIGCRFP--YLEASDYKDFYICVNGSENKPIRSY 227
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 172 YGPWTE-----ECOYSKDTLSRNTACFPRTPIHAKARDLAVHVGSSNHATIKPFD 225
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 228 FTFQQLNIVKPLPVYLTFTRESSECEIKLKWISPLGPIPARCFDYELI-REDDTLVTA 286
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 226 QLFTQALDQNPMDVATEGS-RLSIQMKPVSAPFPHCFEYEVKICNTKDYQVEK 284
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 287 TVENETYLKTTNTRQLCFVVRSKVNIYCSDDGIWSEWSDKQWEGEDLSKTKTLR-FW 345
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 285 TTTNA--FVSTDGVSKYSIOVRAAVSPHCRAMGLWSEKWS-QPYVVGKE--KKPIAGWFL 339
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 346 LPFGFILLIVFVGLLRKPNTPKMP 374
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 340 IITLPAVLFCILLIFFELCRHYHLWTKMFP 368
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |

RESULT 5
Q15469 PRELIMINARY; PRT; 333 AA.
ID Q15469
AC Q15469
RT "Biological activities of interleukin-13 on bovine lymphocytes:
01-NOV-1996 (TREMBlrel. 01, Created)
01-NOV-1996 (TREMBlrel. 01, Last sequence update)
01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSILSR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE-92121815; PubMed-1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X62156; CAA44081.1; -.
DR InterPro; IPR002996; -.
DR DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 13.9%; Score 292; DB 4; Length 333;
Best Local Similarity 28.0%; Pred. No. 3.2e-18;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPQDFEIVDPGLYLYLQWQPLSLDHPKECTVEYELKYRNISETWTKITIT 86
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 25 DEKISLLPPVNETIKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAKPEDDYETRIT 82
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 87 KNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVOSSWAEITYWISPOGIPETKVQDMDCV 146
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 83 ES---KCVTILHKGFSAVSRTILO---NDHSLASSWASAEHL-APPGSPGTSIVNLCT 135
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 147 -----YNNWQYLL-CSWKPGIGVLLDTNLYFY---WYEGLDHALQCVDIKAD 191
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 136 TWTEDNYSLRSYQVSLHCTWLVGTDAPEDTQFLYRYGSWTE-----ECOYSKDT 189
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSENKPIRSYFTFQQLNIVKPLPVYLTFTTR 248
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 190 LGRIACWFPTFLSKGRDLAVLVNGSSKHSAIRPDFQLFALHAIQINPLNVTAEI 249
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 249 ESSECEIKLKWISPLGPIPARCFDYELIREDDTTLVTVATVENETTYLTKTNETRQLCFV 308
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 250 EGT-RLSIQWKEKPVSAFPHCFDYEVKIHNTRNGYLOIEKLMTNWAFISIIDLSKYDVQV 308
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 309 RSKVNIYCSDDGIWSEWS 326
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |
QY 309 RAAVSSMCREAGLWSEWS 326
Db : : : | : | : : : | : | : : : | : | : : : | : | : : : | : |

RESULT 6
Q97597 PRELIMINARY; PRT; 349 AA.
ID Q97597
AC Q97597
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.L., Hirano A., Brown W.C., Estes D.M.;
RT "Biological activities of interleukin-13 on bovine lymphocytes:

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RT. implications for signaling through IL-13ral.
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF074402; AAC98147.1; -
 DR InterPro: IPR002996; -
 DR InterPro: IPR003532; -
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 349
 FT SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 12.6%; Score 264.5; DB 6; Length 349;
 Best Local Similarity 24.4%; Pred. No. 9.9e-16;
 Matches 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;

QY 53 WQPLSLDHFKECTVEYELKYRNTGSETWTKTIITKNLHYKDFDLNKGIEAKIHTLLPMQ 112
 DB 18 WNPPEGAS--PNCSLKY---FSHFGNKQDKKIAPET-HRSKEVPLNERICLQVGS---Q 67
 QY 113 C-TNGSEVQSSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTYNL 171
 DB 68 CSTNESEKPSILBECF-SPEGDPESAVALQCIWHNLRYMKCTWLPGRNASPDNYIL 126
 QY 172 FYWYEGDLHALQVDYIKADQNGICGRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFT 229
 DB 127 YYHNSLGLKILQCFNRYR-EGQIACSFNLTKVKDSFEQHSVQVYRDNAGKISPSFNI 185
 QY 230 FQNLQYKPLPPVLTTRSSCEIKLWSIPLGPIPARCFDYIEIREDDTTLVATVE 289
 DB 186 VPLTSHVKP-DPSHIKNSLFQNGDLYQWNTPNQ-FSQCLCYEVEVINSHA----- 235
 QY 290 NETVLTKTNETR-----QICFVV-----RSKVNIYC-SDDGWS 323
 DB 236 -ETHDIYVEAKQNTFEFEGNLEGTCFVWGVLPDPTLTVIRVIRKTKLCYEDDKLWS 294
 QY 324 EWSKQKQWEGSDLSKTKILLRFLWLPFGFILIVFVTGLLL 363
 DB 295 NWS-----QAMSIGOKANQTFYIT--TLIIIPVIVAAVI 327

RESULT 7

Q9UDY5 Q9UDY5 PRELIMINARY; PRT; 279 AA.
 AC Q9UDY5;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wada M., Hisano T., Kuwano M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U81380; RAD00511.2; -
 DR HSP: P40189; IBOU
 DR InterPro; IPR002996; -
 DR InterPro; IPR003532; -
 DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;

Query Match 11.5%; Score 241.5; DB 4; Length 279;
 Best Local Similarity 27.7%; Pred. No. 8.6e-14;
 Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;
 QY 11 LYTFELISTTGCTSSSTDEIKVNPQDFEIVDPGLGYLYLQWOPPLSLDHFKECTVEY- 69
 DB 10 LWALLCAGGGGGGGAAPTETQPPVTNLSVSENLCVITWNPPEGAS--SNCSLWIF 67

QY 70 ----ELAYRNIGSETWTKTIITKNLHYKDFDLNKGIEAKIHTLLPMQ--TNGSEVQSSWA 124
 DB 68 SHFGDKQDKKIAPETRRSI-----EVLNERICLQVGS-----CSTNESEKPSILV 114
 QY 125 ETTYWIS-POGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTYNLFWYEGDLHALQ 183
 DB 115 EKC--ISPPEGDPESAVALQCIWHNLRYMKCSWLPGRNTSPDNTYLYYWHRSLEKIHQ 172
 QY 184 CVDYIKADQNGICGRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFTFQNLQYKPLPP 241
 DB 173 C-ENIFREGQYFGCSFDLTKVKDSFEQHSVQIMVKDNAGKIKPSPFNTVPLTSRVKPDPP 231
 QY 242 --VLTTRSSCEIKLWSIPLGPIPARCFDYIEIREDDT 281
 DB 232 HIKNLSFHD--DLVYOVENPQNF--SRCLFYEVVNNSTQ 269

RESULT 8

Q9DEQ1 Q9DEQ1 PRELIMINARY; PRT; 363 AA.
 AC Q9DEQ1;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT)
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang J., Secombes C.J.;
 RT "Cloning and expression of the first non-mammalian cytokine receptor
 common gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ276623; CAC09429.1; -
 KW Receptor.
 FT NON_TER 1
 FT SEQUENCE 363 AA; 41861 MW; DF69B2E3E3EA06D3 CRC64;

Query Match 9.4%; Score 197.5; DB 13; Length 363;
 Best Local Similarity 21.9%; Pred. No. 1.1e-09;
 Matches 61; Conservative 56; Mismatches 134; Indels 27; Gaps 9;
 QY 97 LNKGIEAKIHTLLPMQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCS 156
 DB 1 IHKYVRVELVTLIPTVIHFDKMGVSW--LFLLSLQGYEAPSTPNVNCILINDYVNCI 58
 QY 157 WKPQIGVLLDTYNLFWYEGDLHALQCVDIKADQNGICGRFPYLEASDYKDFYICVNG 216
 DB 59 WSE--QSIPEVNFNFTFSRFRKONMEECTTYLQEEYAVGVCRLSYDKSDRFR----- 108
 QY 217 SSENKPIRSSYFTFO---LQNIYKPLPPVLTTRSSCEIKLWSIPLGPIPARCFDYE 273
 DB 109 TLTKLVHQNNSYVDHNLKSMVKLYPPNLSVEMNKDPELNLYNNKNTF---CIESE 165
 QY 274 IEIREDDTTLVATVENE--TYTLKTTNETRQLCFVVRKSNVYICSDDGISEWSEKDCWE 332
 DB 166 VYVRINSDKWKTSTPSKEQRYAVAFPLKSSRYEFQVRYARVNDMCGESEFWSEWSQPIQWD 225
 QY 333 G-----EDLSKKTLLRFLWP-FGFILILVIFVTGLLL 363
 DB 226 SMGNNITDISGSS-MSVWKPVLVSLVGTMTLFIACML 262

RESULT 9

Q9PTIO Q9PTIO PRELIMINARY; PRT; 611 AA.
 ID Q9PTIO;
 AC Q9PTIO;
 DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE PROLACTIN RECEPTOR A.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087225; PubMed=10618394;
 RA Huang H., Brown D.B.;
 RT "Prolactin is not a juvenile hormone in Xenopus laevis
 RT metamorphosis."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
 DR EMBL; AF193800; AAF05776.1; -.
 DR HSP; P16471; IBP3
 DR InterPro; IPR001777; -.
 DR InterPro; IPR002996; -.
 DR InterPro; IPR003528; -.
 DR Pfam; PF00041; fn3; 1.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
 DR SMART; SM00060; FN3; 1.
 DR RECEPTOR.
 KW SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;
 SQ SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;

 Query Match 8.98; Score 187; DB 13; Length 611;
 Best Local Similarity 26.18; Pred. No. 1.8e-08;
 Matches 70; Conservative 41; Mismatches 117; Indels 40; Gaps 11;

 QY 127 TWISPOGIPETKVDQDCVYNNQYLCSMKPGIGVLLDFTNLYNLFYWEGLDHALQCV 186
 DB 22 TVSLNAQSLPKPKVID-KRSYKAVTSCWKKPGSDGLPTNYSLLYRKENDPKIYEC 80
 QY 187 YKADGONIGCRFPYLEADYKDYICVNGS-----SENKPIRSSYFTFQLQNIKVL 239
 DB 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYVNTALNGSNVDSDESDVTY-----IVQ 131
 QY 240 PPVILTFRESS-CEIKLWSIPGLPIPARCFD-----YEIEIREDDTTLVTATVE 289
 DB 132 PPTNVSLAVESGHDLKLK-----LPPAMVDVQSGWMLTLKYEVRYKEEKEQWEAHLV 185
 QY 290 NETYTLKTTNETROLCFVRSKVNIGS-DDGIWSEWSKQCEGEDLSKKTLLRFLWLPF 348
 DB 186 GNQLKLKFLGLTPGNGVYVQ---VRCKPSGHSWSESTESYIPIGGGKKTDLTLMISI 241
 QY 349 GFI--LILVIFVTGLLRKPNTPYKMP 374
 DB 242 GALSAVICLTMIWTMALKRCSLMSCILP 269

 RESULT 11
 Q64146 PRELIMINARY; PRT; 896 AA.
 AC Q64146;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
 GN RIL-3R<BETA>.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95370942; PubMed=7643220;
 RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
 RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
 RT microglia and its mRNA expression in vivo."
 RL J. Neurosci. 15:5800-5809(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RA Gebicke-Haerter P.J.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; S79263; AAB35068.1; -.
 DR EMBL; AJ000555; CAA04186.1; -.
 DR InterPro; IPR000282; -.
 DR InterPro; IPR001777; -.
 DR InterPro; IPR002996; -.
 DR InterPro; IPR003531; -.
 DR Pfam; PF00041; fn3; 2.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 DR SMART; SM00060; FN3; 1.
 KW Signal.
 FT NON_TER 896
 FT NON_TER 896
 SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE PROLACTIN RECEPTOR A.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087225; PubMed=10618394;
 RA Huang H., Brown D.B.;
 RT "Prolactin is not a juvenile hormone in Xenopus laevis
 RT metamorphosis."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
 DR EMBL; AF193800; AAF05776.1; -.
 DR HSP; P16471; IBP3
 DR InterPro; IPR001777; -.
 DR InterPro; IPR002996; -.
 DR InterPro; IPR003528; -.
 DR Pfam; PF00041; fn3; 1.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
 DR SMART; SM00060; FN3; 1.
 DR RECEPTOR.
 KW SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;
 SQ SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;

 Query Match 8.98; Score 187; DB 13; Length 611;
 Best Local Similarity 26.18; Pred. No. 1.8e-08;
 Matches 70; Conservative 41; Mismatches 117; Indels 40; Gaps 11;

 QY 127 TWISPOGIPETKVDQDCVYNNQYLCSMKPGIGVLLDFTNLYNLFYWEGLDHALQCV 186
 DB 22 TVSLNAQSLPKPKVID-KRSYKAVTSCWKKPGSDGLPTNYSLLYRKENDPKIYEC 80
 QY 187 YKADGONIGCRFPYLEADYKDYICVNGS-----SENKPIRSSYFTFQLQNIKVL 239
 DB 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYVNTALNGSNVDSDESDVTY-----IVQ 131
 QY 240 PPVILTFRESS-CEIKLWSIPGLPIPARCFD-----YEIEIREDDTTLVTATVE 289
 DB 132 PPTNVSLAVESGHDLKLK-----LPPAMVDVQSGWMLTLKYEVRYKEEKEQWEAHLV 185
 QY 290 NETYTLKTTNETROLCFVRSKVNIGS-DDGIWSEWSKQCEGEDLSKKTLLRFLWLPF 348
 DB 186 GNQLKLKFLGLTPGNGVYVQ---VRCKPSGHSWSESTESYIPIGGGKKTDLTLMISI 241
 QY 349 GFI--LILVIFVTGLLRKPNTPYKMP 374
 DB 242 GALSAVICLTMIWTMALKRCSLMSCILP 269

 RESULT 10
 Q9IBF6 PRELIMINARY; PRT; 611 AA.
 AC Q9IBF6;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE PROLACTIN RECEPTOR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
 RT "Cloning of a cDNA for Xenopus prolactin receptor and its
 RT metamorphic expression profile."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030443; BAA90400.1; -.
 DR InterPro; IPR001777; -.

Query Match 8.5%; Score 178; DB 11; Length 896;
 Best Local Similarity 21.4%; Pred. No. 1.8e-07;
 Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLATGCL--YT-FLISTFTGCTSSDREIKVN-----PPQFEIVDPGYLGYL 49
 DB 94 CVPKRCVLPYTFQSVSKEDYYSLQPDRLSLHLVPLAQHVQPPPKDISPSG--DHF 151
 QY 50 YLQWQPLP---SLDHECTVEYELKYNIGSETWKTIIKNLHYKDGFDLNGIEAKIH 106
 DB 152 LKWSVPLGDAQVSLLSOKDIQFEVAKQL-QDSWED--ASSLH-----TCNLWVTLEPK 203
 QY 107 TLLP-----WQCTNSSEVQ---SSWAEYTWISPOGIPETKVQDMDCVYNNWYLL 154
 DB 204 LFLPNSIYVARVRAQLAGSSLSGRPSGWSPEVHWDSPTE-DRARPQNLOCFDGIQSLN 262
 QY 155 CSWPKPGVLLDYNLIFYWEGLDHALQVDYIKACQNGICGRFPYLEASDYKDFYICV 214
 DB 263 CSWEVWTKVTDVSFGFLFYSSPRAGEKKGSPVVK-----LOASRYTRYHCSL 311
 QY 215 NGSENKPIRSSYFTFOLQ-----NIVKPLPP-VLTFRESSCEIKLKWISPL 262
 DB 312 NVSD---PAHSQYTVSVKRLQKQFTESFNHIOQNNPTLMTKNRDS---YSLHWETQK 365
 QY 263 GPIPARCFDYEIEIR-----EDDTTLVTATVENETYTLKTTNETROLCFVYRSKVNIYC 316
 DB 366 MSYFFIQHAFQVQYKKLDRWEDSKT---ENLNAHSMDLPOLEPGTSCYCARVRVKIP 421
 QY 317 SDDGIWSEWSKQWEGEDLSKTLRLFWLPGFILLIVFTVGLLL 363
 DB 422 EYKGLWSEWSNCTWT-TDWMVMTPL---WI-----VLILVFLILFTFL 460

RESULT 12
 Q9PTH9 PRELIMINARY; PRT; 611 AA.
 AC Q9PTH9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE PROLACTIN RECEPTOR B.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang H., Brown D.D.;
 RL MEDLINE=20087225; PubMed=10618394;
 RT "Prolactin is not a juvenile hormone in Xenopus laevis
 metamorphosis".
 RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
 DR EMBL; AF193801; AAF05777.1; -;
 DR HSP; P16471; IAP3.
 DR InterPro; IPR001777; -;
 DR InterPro; IPR002996; -;
 DR InterPro; IPR003528; -;
 DR Pfam; PF00041; fn3; 2.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
 DR SMART; SM00060; FN3; 1.
 KW Receptor.
 SQ SEQUENCE 611 AA; 68481 MW; CAC658A8A66B313 CRC64;

Query Match 8.3%; Score 174.5; DB 13; Length 611;
 Best Local Similarity 26.4%; Pred. No. 2.3e-07;
 Matches 68; Conservative 39; Mismatches 120; Indels 31; Gaps 11;

QY 131 SPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNLYNLFYWEGLDHALQVDYIKA 190
 DB 29 SPPGKPEI-----IKRSYKVTFCWKKPASDGLPTNYSLLYRKENDPKIYECPDY-ET 83

QY 191 DGONIGCRFPYLEASDYKDFYCVNGS-----SENKPIRSSYFTFOLQNIKVPPLPVY 243
 DB 84 SGLN-SCYFDKAKHTSFWFVHIYVNAATLGSNSVSELSVDITY-----IVETYPPTN 135
 QY 244 LTTRESS-CEIKLWKSIP-LGPIPA--RCFDYEIEIREDDTTLVTATVENETYTLKTTN 299
 DB 136 LSTVEDGHDLVLLKVPDPMDADVQSGWLTLYKEVRLKEKEQWEAHSVGNQLKLKLYG 195
 QY 300 ETROLCFVRSKVNIYCS-DDGIWSEWSKQWEGEDLSKTLRLFWLPGFI--LILVI 356
 DB 196 LTPGNNVVO-----VRCKPDSGHWSEWSQESYTIQLGGKKTDLMLWISVGTLSAVICLT 251
 QY 357 FVTGCLLLRKNTYPKMIP 374
 DB 252 MIWTMLKRCVSMSCILP 269

RESULT 13
 Q57519 PRELIMINARY; PRT; 881 AA.
 AC Q57519;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE GP130P1.
 GN XGP130.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen J., Grace A., Chien K.R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF041845; AAC09531.1; -;
 DR HSP; P40189; 1BQU.
 DR InterPro; IPR001777; -;
 DR InterPro; IPR002996; -;
 DR InterPro; IPR003529; -;
 DR Pfam; PF00041; fn3; 4.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR SMART; SM00060; FN3; 1.
 SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 8.2%; Score 173.5; DB 13; Length 881;
 Best Local Similarity 25.0%; Pred. No. 4.5e-07;
 Matches 75; Conservative 37; Mismatches 115; Indels 73; Gaps 14;

QY 68 EYELKYRNIGSETWKTIIKNLHYKDGFDLNGIEAKIHLLPWCQINGSEVQSSWAETT 127
 DB 74 QYELNQTTSVTENLTLLN-----SPLTCNVMSGHV-----ANTL 111
 QY 128 YWI-SPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNLYNLFY-W-YEGLDHALQ 184
 DB 112 YGIFFTLGLPDKPTNLTCTVYNQDNLTCTWDGPRPTNLTPTNLTSLHRAHFGANY---- 167
 QY 185 VDIKADQNGICGRFPYLEASDYKDFYCVNGSENKPIRSSYFTFOLQNIKVPPLPVY-- 243
 DB 168 -----CRGANNSTIHSPPGFQYIDTTFQVEATNELGIQKSETLIDPVNIVKPNPQLS 222
 QY 244 -LTTRESSCEIKLWKSIPLGPI-----PARCFDYEIEIREDDTTLVTATVENET 292
 DB 223 ELISSELPLNALKIEWKNPITNAFNLNKYNIRYRPVKTDWEM-VPEEDT-----ASRDS 276
 QY 293 YTLK-----TTNETROLCFVYRSKVNIYCSDDGIWSEWS--KQCW-----EGEDLSK 339
 DB 277 FTLODLLPNTVIEVSIRC-----LHKDGHGFWSDMSLKKQVTEAPPSPRGPDWKK 328

RESULT 14

Q921A0 Q921A0 PRELIMINARY; PRT; 890 AA.

AC Q921A0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR BETA CHAIN.
GN IL5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;

RN [1]
RP SEQUENCE FROM N.A.
RA Logsdon N.J., Graham A., Scott C.W.;
RT "Guinea pig IL5 receptor beta chain."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U94688; AAC77520.1; -
DR InterPro; IPR000276; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 890 AA; 96578 MW; D43FBICA88525536 CRC64;

Query Match 8.18; Score 170; DB 11; Length 890;
Best Local Similarity 23.88; Pred. No. 9.4e-07;
Matches 88; Conservative 53; Mismatches 144; Indels 84; Gaps 21;

Qy 34 PPQDFEIVDPGLYLYLOWQPPSLDH---FKECTVEYELKYRNIGSETWKTITKNLH 90
Db 138 PPQDVQINTSG--DQVLTWSVALEGPHTSWLSQRLDEFEVYKRL-HEPWESAST--LH 192
Qy 91 YKDG-----FDLNGIEAKIHTLLPWQCTNGSEVO---SSWAETTYWISPOGIPETK 139
Db 193 SNSSOALGPELPFLPSSYVARVTRL---ARGSGFSRPSQMSPEVSWSSQPG-DQAQ 247
Qy 140 VQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDHALQ-CVDYIKRADGONI--- 195
Db 248 PQNLQCVFDGARTLCSNEVRSQVTSVSGFLY-RSSLDAGEQECPOVQKEELHDIYTR 306
Qy 196 -GCRPFYLEADYKDFYICVNGSSSENKPIRSYFTFQLNIVKPLPPVYLFTRESSCEI 254
Db 307 HSCQIRVSNRPHSQYTVTRPNRGEKFIKSA-----NHIQMAAPT-LNVTKDGD-TY 357
Qy 255 KLKWSIPLGPIPARCF-----DYEIEIREDDTLTATVENETVTK----- 296
Db 358 SLRW-----VTKMYSHIENTEIQYR---TAGDRWENSKTETLKNAHNMPPLPLEP 407
Qy 297 -TTNETROLCFVWRSKVNIYCSDDGINSWSDKQWGEDLSKKTLLRFW-LPFGFILIL 354
Db 408 ATTVLAR-----VRVKPSPGGAYNGINSEWSEQRWTTD-----WALPTWVLALV 452
Qy 355 VIFVTGLLL 363
Db 453 LVLVTALL 461

RESULT 15
Q9N0J7

ID Q9N0J7 PRELIMINARY; PRT; 622 AA.
AC Q9N0J7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Dairymple A., Edery M., Jabbour H.;
RT "Sequence and functional characterisation of the marmoset monkey
RT (Callithrix jacchus) prolactin receptor: comparative homology with the
RT human long form prolactin receptor."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ272217; CAB75847.1; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW SIGNAL; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 622 PROLACTIN RECEPTOR.
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6CD6DB6 CRC64;

Query Match 7.98; Score 167; DB 6; Length 622;
Best Local Similarity 28.88; Pred. No. 1.1e-06;
Matches 61; Conservative 26; Mismatches 91; Indels 34; Gaps 10;

Qy 131 SPQGIPTKVDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCVDIKA 190
Db 26 SPQKPEI----FKCRSPNKETFTCWWRPGADGGLPTNYSLAYHKEGKFTHECPDYY-T 80
Qy 191 DQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLNIVKPLPPVYLFTTRES 250
Db 81 GGPN-SCHFGKQYTSMMRTYIITVNATNMGSTLSDEIYVDVTIVEPDPPLNVV----- 134
Qy 251 SCEIK-----LKWSIP-LGPIPARCFD--YEIEIREDDTLTATVENETVTLKT 297
Db 135 -VEYKQPEDKKPYLWIKRSPPTLIDLKTGFTLLYEIQLKPENAE-----EWETHFAGQ 187
Qy 298 TNETROLCFVVRSK--VNIYCS-DDGIWSEWS 326
Db 188 QTFKVLSLHPGQKYLQVQCKPDHGYWSSWS 219

Search completed: September 1, 2001, 19:15:52
Job time: 524 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:55 ; Search time 43.66 Seconds
(without alignments)
587.971 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLAIIGCLYFLISTTF.....DDGIWSEWSKQWEGEDLS 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 293.5 | 15.7 | 420 | 2 S21052 | interleukin-5 rece |
| 2 | 292 | 15.6 | 335 | 2 A40267 | interleukin-5 rece |
| 3 | 254 | 13.6 | 831 | 2 JQ1655 | prolactin receptor |
| 4 | 229 | 12.2 | 415 | 2 S12357 | interleukin-5 rece |
| 5 | 210.5 | 11.2 | 830 | 2 I50455 | prolactin receptor |
| 6 | 202.5 | 10.8 | 369 | 2 A42565 | interleukin-2 rece |
| 7 | 199.5 | 10.7 | 373 | 2 A55718 | interleukin-2 rece |
| 8 | 198.5 | 10.6 | 369 | 2 I49280 | interleukin-2 rece |
| 9 | 179 | 9.6 | 878 | 1 A40091 | interleukin-3 rece |
| 10 | 165 | 8.8 | 310 | 2 A29884 | prolactin receptor |
| 11 | 165 | 8.8 | 412 | 2 A41070 | prolactin receptor |
| 12 | 165 | 8.8 | 581 | 2 I45971 | prolactin receptor |
| 13 | 165 | 8.8 | 610 | 2 A34631 | lactogen receptor |
| 14 | 165 | 8.8 | 610 | 2 A36116 | prolactin receptor |
| 15 | 165 | 8.8 | 896 | 2 I56363 | interleukin-3 rece |
| 16 | 160 | 8.5 | 897 | 1 A39255 | cytokine receptor |
| 17 | 159 | 8.5 | 292 | 2 I77525 | prolactin receptor |
| 18 | 159 | 8.5 | 303 | 2 I77524 | prolactin receptor |
| 19 | 159 | 8.5 | 608 | 2 I53269 | prolactin receptor |
| 20 | 155.5 | 8.3 | 896 | 1 A35782 | cytokine receptor |
| 21 | 151 | 8.1 | 622 | 2 A40144 | prolactin receptor |
| 22 | 150.5 | 8.0 | 917 | 2 I49699 | glycoprotein 130 - |
| 23 | 147 | 7.8 | 616 | 2 A30304 | prolactin receptor |
| 24 | 133.5 | 7.1 | 333 | 2 S13684 | granulocyte-macrop |
| 25 | 133.5 | 7.1 | 378 | 2 S50040 | granulocyte-macrop |
| 26 | 133.5 | 7.1 | 400 | 2 S06945 | granulocyte-macrop |
| 27 | 130.5 | 7.0 | 378 | 2 A40266 | interleukin-3 rece |
| 28 | 129 | 6.9 | 150 | 2 B34631 | lactogen receptor |
| 29 | 128 | 6.8 | 630 | 2 I51086 | prolactin receptor |

30 126.5 6.8 918 2 A36337 membrane glycoprot
31 123.5 6.6 1097 2 S17308 leukemia inhibitor
32 122.5 6.5 286 2 S50039 granulocyte-macrop
33 112.5 6.0 1630 2 C41214 protein-tyrosine-p
34 111.5 6.0 1557 2 D41214 protein-tyrosine-p
35 109.5 5.8 918 2 A44257 interleukin-6 sign
36 109.5 5.8 26926 1 I38344 titin, cardiac mus
37 106 5.7 634 2 S33339 somatotropin recep
38 105.5 5.6 1825 2 T32828 hypothetetical prote
39 105 5.6 837 2 A34898 granulocyte colony
40 104.5 5.6 6805 2 S20901 titin - rabbit (fr
41 104 5.6 771 2 B38252 granulocyte colony
42 104 5.6 783 2 JH0329 granulocyte colony
43 104 5.6 863 2 C38252 granulocyte colony
44 100 5.3 817 2 A48721 titin, muscle - ch
45 99.5 5.3 638 2 S12136 somatotropin recep

ALIGNMENTS

RESULT 1

S21052

interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence.revision 10-Nov-1995 #text.change 01-Dec-2000
C;Accession: S21052; S21050: S21053; A46175; S78106; S78107
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor.
A;Reference number: S21050; MUID:92121815
A;Accession: S21052
A;Molecule type: DNA
A;Residues: 1-420 <MUR>
A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A;Experimental source: clone lambda h5R.12
A;Accession: S21050
A;Molecule type: DNA
A;Residues: 1-395, 'I' <MU2>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A;Experimental source: clone lambda h5R.27
A;Accession: S21053
A;Molecule type: mRNA
A;Residues: 1-332, 'K' <MU3>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A;Experimental source: clone lambda h5R.25
R;Ravener, J.; Tulpens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum

A;Reference number: A46175; MUID:92357767
A;Accession: A46175
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 333-420 <TAV>
A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R;Murata, Y.
Submitted to the EMBL Data Library, July 1991
A;Reference number: S78106
A;Accession: S78106
A;Molecule type: DNA
A;Residues: 1-128, 'I', 130-395, 'I' <MUW>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R;Murata, Y.
Submitted to the EMBL Data Library, September 1991
A;Reference number: S78107
A;Accession: S78107
A;Molecule type: mRNA
A;Residues: 1-128, 'I', 130-332, 'K' <MU4>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

A:Molecule type: mRNA
A:Residues: 1-415 <TAK>
A:Cross-references: GB:D90205; NID:G220465; PIDN:BAAL4231.1; PID:G220466
C:Keywords: cytokine receptor; transmembrane protein

Query Match 12.2%; Score 229; DB 2; Length 415;
Best Local Similarity 24.8%; Pred. No. 6.4e-11;
Matches 79; Conservative 56; Mismatches 135; Indels 48; Gaps 13;

Qy 34 PPQDFEIVDPGYLYLQWPPISLDHFKECTVEYELKYNIGSETWTKTITKNLHYKD 93
Db 29 PVVNFETIKATG-LAQVLLHDPNPDOEQ-RHVDLEYHVKNAPQOEDEYTRKTES---KC 83
Qy 94 GFDLNGTEAKIHTLLPWCQTNNGSEVQSSWAETTYWISPOGIPETKVKQDMDCVYN---- 149
Db 84 VTLPHGFAASVRTLK---SSHTEGLASSWSAEL-KAPPGSPGTSVNLCTHTTVVSS 139
Qy 150 -----WQY-LICSWKPGIGVLLDTNMLFYWYEGLDHALQCVDYIK-ADGONIGCRPP- 200
Db 140 HTHLRPPYQVSLRCLWVGKDAPEDTQYLYYRFGVLTE--KCQEYSRDLNLRNTACHFPR 197
Qy 201 YLEASDYKDYICVNGSENKPIRSSTFTFQLOINVKPLPPVYLFTFRESSCEIKLWKS 259
Db 198 TFINSKGEQLAVHINGSKRAAIKPFQLESPLAIDQVNPNNVTVEISN-SLYIQWE 256
Qy 260 IPLGPAPARCDFYEIREDD-----TTLVTATVENETTLTKTNETRQLCFV 308
Db 257 KPLSAPPDHCENYELKIYNTKNGHIQKEKLIANKPIFSKIDVSTYSIQ-----V 305
Qy 309 RSKVNIYCSDDGIWSEWS 326
Db 306 RANVSSPCRMFGWSEWS 323

RESULT 5
150455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C:Accession: 150455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: 150455; MUID:94283267
A:Accession: 150455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:G466381; PIDN:AAA20646.1; PID:G466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 11.2%; Score 210.5; DB 2; Length 830;
Best Local Similarity 24.7%; Pred. No. 4.8e-09;
Matches 86; Conservative 47; Mismatches 156; Indels 59; Gaps 14;

Qy 18 TFGCTSSSDTEIKVNPQDFEIVDPGYLG-----DPQYVDVTSIVQDPAPVNLSELTASTVYLLAKW 150
Db 97 TTYNTVMAINEIGSNSS-----DPQYVDVTSIVQDPAPVNLSELTASTVYLLAKW 150
Qy 54 QPPLSLDFHFKECTV-EYELKYNIGSETWTKTITKNLHYKGFQDLNKGIEAKIHTLLPQ 112
Db 151 SPPPLADVTSNHYRYELRLKPEKEWETV---SVGQYQYKYNR-LOAGVKYVQVQR 206
Qy 113 CTNGSEVQSSWAETTYWISPOG-IPETKVKQDMDCVYNWYLLCSWKPGIGVLLDTNVL 171
Db 207 CVLDIGEMSESSRRHIHPNGESPPEKPTTIKCRSPEKETFTCMWRKPGSDGGHPNTTL 266
Qy 172 FYWYEGLDHALQCVDYIKADGONIGCRPPYLEASDYKDFYICVNGSENKPIRSSTFT 231

Db 267 LYSKEGEBRVYECOPY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLVYD 324
Qy 232 LQNIKVPPLPPVYLFTRESSCEIK-----LKWS-ITLGPIPA--RCFDYEIREDDTITLV 284
Db 325 VTYIVQTDPPVNVTLKTKTYNRKPYLVLTWSPPLADVRSGWLTLDYELRLKPEEA--- 381
Qy 285 TATVENETITLTKTNETRQLCFV-----RSKVNIYCSDD--GIWSEWS 326
Db 382 -----EWEETIFVQGOHYKMFSLNPGKKYIVQIHCKRDPDHGWSSEWS 424

RESULT 6
A42565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A42565; A46591; I54332
R:Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: GB:D11086; NID:G303611; PIDN:BAA01857.1; PID:G219890
A:Experimental source: MOLT beta lymphoid cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:L12183; NID:G307056; PIDN:AAA59145.1; PID:G307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.;
Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11
A:Reference number: I54332; MUID:94004847
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L19546; NID:G349631; PIDN:AAC37524.1; PID:G349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:I34807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A:Note: defects are associated with an X-linked form of severe combined immunodeficie
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.8%; Score 202.5; DB 2; Length 369;
Best Local Similarity 24.8%; Pred. No. 7.4e-09;
Matches 61; Conservative 45; Mismatches 111; Indels 29; Gaps 9;

Qy 97 LNKIGTEAKIHTLLPWCQTNNGSE-VQSSWAETTYWISPOGIPETKVKQDMDCVYNWYLLC 155
Db 19 LGVGLNTILT-----PNGNEDTTADFFLTMPDLSVSTLPLPEVQCFFVVEYVNC 72
Qy 156 SW-----KPGIGVLLDTNMLFYWYEGLDH--ALQCVDYIKADGONIGCRPPYLEASDY 207
Db 73 TWNSSEPOPP-----TNLTLYHWYKNSDNDKVKCKSHLYFSEITSGCQLQKKKEIHL 125
Qy 208 KDFYICVNGSENKPIRSSTFTFQLOINVKPLPPVYLFTFRESSCEIKLWKSIPLGPIPA 267
Db 126 QTFVYQLQDPRE--PRQATQMLKLNVLIPWAPENLTLHLKLSQLELNWN---NRLN 180
Qy 268 RCFDYEIRED-DTTLVTATVE-NETVTLTKTNETRQLCFVVRSKVNIYCSDDGIWSEW 325

Db 181 HCLEHLVQRTDWDHSHWTEQSDVYRHKEFLPSVDCQKRYTFVRSRFPLCGSAQHWSEW 240
QY 326 SDKQCW 331
Db 241 SHPIHW 246
RESULT 7
A:Species: Canis lupus familiaris (dog)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
R:Accession: A55718
R:Henrich, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg, P.
Genomics 23, 69-74, 1994
A:Title: IL-2R gamma gene microdeletion demonstrates that canine X-linked severe combined
A:Reference number: A55718; MUID:95130114
A:Accession: A55718
A:Status: preliminary
A:Residues: 1-373 <HEN>
A:Cross-references: GB:U04361; NID:9517411; PIDN:AA048403.1; PID:9517412
A:Superfamily: Interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication
Query Match 10.78; Score 199.5; DB 2; Length 373;
Best Local Similarity 26.98; Pred. No. 1.3e-08;
Matches 63; Conservative 40; Mismatches 96; Indels 35; Gaps 10;
QY 115 NGSE-----VQSSWAETTYWISQGIPTKQVDMDCVYNNWOYLCSW-----KPGI 161
Db 31 NGNEDITDFELTATPSET---LSVSSLPLPEVQ---CFVENVEYMNCTWNSSEPRP-- 82
QY 162 GVLLDTNLYFWYEGE--DHALQCVDIKADGONIGCRFFYLEASDYKDFYICVNGSSE 219
Db 83 -----TNLTLYHWYKNSNDKRVQCGHFLFSREVTAGWLQKEITHLYETVTVQLRDPR 137
QY 220 NKPIRSYFTFQOLNIVKPLPPVLTFTRESSCEIKLKWSTPLGPIPARCFDYIEIRED 279
Db 138 --PRQSTQKQLKQNLVPAWENLTNLNLSQLELSWS---NRHLDHCLHVVVQVRSD 192
QY 280 -DTLVATVENE-ETYLTKTNTETROLQCFVVRKVNIVCSDDGIWSEWSDKQCW 331
Db 193 WDRSWTEQSDVHRNFSFLPSVDCQKRYTFVRSRFPLCGSAQHWSEWHPH 246
RESULT 8
Interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R:Caio, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) g
A:Reference number: A47514; MUID:93391374
A:Accession: I49280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <CAO>
A:Cross-references: EMBL:U21795; NID:9727349; PIDN:AAA64279.1; PID:g727350
A:Accession: A47514
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of funct
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUN>
A:Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma cha
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosoma
A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2R gamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet
eptors.
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily: interleukin-2 receptor gamma chain
F:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-369/product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TM>
F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 10.68; Score 198.5; DB 2; Length 369;
Best Local Similarity 26.5%; Pred. No. 1.6e-08;
Matches 54; Conservative 38; Mismatches 95; Indels 17; Gaps 7;
QY 136 PETKVQDMDCVYNNWOYLCSW-----KPGIGVLLDTNLYFWYEGLDHAL--QCVDYIK 189
Db 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPPQA-----TNLTLYRYKVSNDNTFQECSHYLF 107
QY 190 ADGONIGCRFFYLEASDYKDFYICVNGSSENKPIRSYFTFQOLNIVKPLPPVYLTFTRE 249
Db 108 SKETSCQIQKEDIQLYQYFVQVL--QDPKQPORRAVKQLNQLNIPRAPENLTLSNL 165
QY 250 SSCBIKLKWSIPLGPIPARCFDYIEIRED-DTFLVATVENE-TYTLTKTNETRQICFV 307
Db 166 SESOLELRWK--SRHIKERGLQYLVQYVRNDRSWTELIVNHEPRFSLPSDELKRYTER 223
QY 308 VRKVNIVCSDDGIWSEWSDKQCW 331
Db 224 VRSRYNPICGSSQWWSKWSQFVHW 247
RESULT 9
A40091
Interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022

Db 183 QTQPKVFDLPQKYLVTQTRCK---PDHGYWSRWSQESSVE 220

RESULT 12

I45971

prolactin receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000

C:Accession: I45971

R:Scott, P.; Kessler, M.A.; Schuler, L.A.

Mol. Cell. Endocrinol. 89, 47-58, 1992

A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin

A:Reference number: I45971; MUID:93246019

A:Accession: I45971

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-581 <SC>

A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618

C:Genetics:

C:Superfamily: cytokine receptor homology

F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 8.8%; Score 165; DB 2; Length 581;

Best Local Similarity 31.3%; Pred. No. 1.4e-05;

Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;

Qy 136 PETKQVDMDCVYVNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCVDIYKADQNI 195

Db 27 PPERPKLVKCRSPGKETFTCWEPGADGGLPTNTLYHKEGETLIHECPDY-KTGGPN- 84

Qy 196 GCRPPYLEASDYKDFYICVNSSENKPIRSSYFTFQLNIVKPLPPVLTFTRESSCEIK 255

Db 85 SCYSKRRHTSWKVVIVTNAINQMGSSDPLVHVHYIIVEPEPPANLLELKHPEDRK 144

Qy 256 ----LKWSIP-LGPIPARCF--DYEIREDDDTLVTATVENET-YTLKTTN-ETQLCF 306

Db 145 PYLWKNSPPTMTDVKSGWFIQYIIRLKPKEAT-----DWETHFTLKQTLKFIENLYP 198

Qy 307 VVRKSVNIYCS-DDGIWSEWS 326

Db 199 GQKYLVIQIRKPDHGYSEWS 219

RESULT 13

A34631

lactogen receptor 1 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 28-Jul-2000

C:Accession: A34631

R:Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.

Biochem. Biophys. Res. Commun. 168, 415-422, 1990

A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA

A:Reference number: A34631; MUID:90241201

A:Accession: A34631

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-610 <ZHA>

A:Cross-references: GB:M34083; NID:g205122; PIDN:AAA79273.1; PID:g205123

A:Note: the authors translated the codon GAG for residue 533 as Gly

C:Superfamily: cytokine receptor homology

F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.8%; Score 165; DB 2; Length 610;

Best Local Similarity 28.5%; Pred. No. 1.5e-05;

Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

Qy 131 SPQGIPTKQVDMDCVYVNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCVDIYKA 190

Db 21 SPPGKPEIH---KCRSPDKETFTCWNNPGTDGGLPTNYSLTYSKEGKTYIECPDY-KT 75

Qy 191 DGQNGICRFPYLEASDYKDFYICVN-----GSENKPIRSSYFTFQLNIVKPLPPVLT 245

Db 76 SGNP-SCFFSKQYTSIWKIYIITVNATNMQGSSSDPL-----YVDVTYIIVEPEPPNLT 129

Qy 246 F---TRESSCEIKLWSSIP-LGPIPARCFDYEIREDDDTLVTATVENET-YTLKTTNE 300

Db 130 LEVQLKDKKTYLWVKSPPPTITDVKTGFTMEYER-----LKPEAEAEWEIHFTHG 182

Qy 301 TROL-----CFVVRKSVNIYCSDDGIWSEWSKQCEW 332

Db 183 QTQPKVFDLPQKYLVTQTRCK---PDHGYWSRWSQESSVE 220

RESULT 14

A36116

prolactin receptor 2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 28-Jul-2000

C:Accession: A36116

R:Shiota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, M.

Mol. Endocrinol. 4, 1136-1143, 1990

A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.

A:Reference number: A36116; MUID:91155946

A:Accession: A36116

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-610 <SHI>

A:Cross-references: GB:M57668; NID:g206366; PIDN:AAA1938.1; PID:g206367; GB:M60728

C:Superfamily: cytokine receptor homology

F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.8%; Score 165; DB 2; Length 610;

Best Local Similarity 28.5%; Pred. No. 1.5e-05;

Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

Qy 131 SPQGIPTKQVDMDCVYVNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCVDIYKA 190

Db 21 SPPGKPEIH---KCRSPDKETFTCWNNPGTDGGLPTNYSLTYSKEGKTYIECPDY-KT 75

Qy 191 DGQNGICRFPYLEASDYKDFYICVN-----GSENKPIRSSYFTFQLNIVKPLPPVLT 245

Db 76 SGNP-SCFFSKQYTSIWKIYIITVNATNMQGSSSDPL-----YVDVTYIIVEPEPPNLT 129

Qy 246 F---TRESSCEIKLWSSIP-LGPIPARCFDYEIREDDDTLVTATVENET-YTLKTTNE 300

Db 130 LEVQLKDKKTYLWVKSPPPTITDVKTGFTMEYER-----LKPEAEAEWEIHFTHG 182

Qy 301 TROL-----CFVVRKSVNIYCSDDGIWSEWSKQCEW 332

Db 183 QTQPKVFDLPQKYLVTQTRCK---PDHGYWSRWSQESSVE 220

RESULT 15

I56563

interleukin-3 receptor beta-subunit - rat

C:Species: Rattus sp. (rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999

C:Accession: I56563

R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.

J. Neurosci. 15, 5800-5809, 1995

A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia

A:Reference number: I56563; MUID:95370942

A:Accession: I56563

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-896 <RES>

A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955

C:Genetics:

A:Gene: rIL-3rbeta

C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology

C:Keywords: cytokine receptor

F:39-235/Domain: cytokine receptor homology <CRS1>

F:253-433/Domain: cytokine receptor homology <CRS2>

```
Query Match      8.8%; Score 165; DB 2; Length 896;
Best Local Similarity 20.5%; Pred. No. 2.4e-05;
Matches 77; Conservative 62; Mismatches 156; Indels 80; Gaps 18;

Qy 5 CIAIGCL--YT-FLISTTFGCTSSSDTEIKVN-----PPQDFEIVDPGYLGYL 49
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Db 94 CVPRCVLPYTOFSYKEDYISLQPDRLSIHLVPLAQHVQPPPKDISISPSG--DHF 151
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Qy 50 YIQWOPPL---SLDHFEKTEYELKYNIGSEWTKTITIKNLHYKDGFDLNGKIEAKIH 106
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Db 152 LKWSVPLGDAQVLSLSQDKIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLEPK 203
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Qy 107 TLIP-----WQCTNGSEVQ---SSWAETTYWISPOGIPETKVQDMDCVYYHNQYLL 154
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Db 204 LFLPNSIYVARVRAQLAPGSSLGRPSGWSPEVHWDSPTE-DKARPQNLQCFDFGIQSLN 262
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Qy 155 CSWKFGIGVLLDTNLYFYWYEGLDHALQCVDYIKADGNIGCRPPYLEASDYKDFYICV 214
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Db 263 CSWEVWTKVTDVSFGLFYSSSPKAGERKCSVVKE-----LQASRYTRYHCSL 311
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Qy 215 NGSSSENKPIRSYFTFQLQ-----NIVKPLPP-VYLTFPRESCEIKLKWISPL 262
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Db 312 NVSD---PAAHSQYTVSVKRLQEQGFIESFNHIQMNPTLNLTKNRDS---YSLHWETQK 365
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Qy 263 GPIPARCFDYETEIR-----EDDTLVTAIVENETYTLKTTNETRQLCFVVRSKVNIYC 316
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Db 366 MSYPTIQHAFQVQYKKLDRWEDSKT-----ENLNHAHSMDLFQLEPGTSYCARVRVKTIP 421
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Qy 317 SDDGIWSEWSDKQCW 331
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
Db 422 EYKGLWSEWSNECTW 436
   | : || | | : | : : || : | | : | : | : | : | : | : | : | : |
```

Search completed: September 1, 2001, 19:07:57
Job time: 124 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:15:54 ; Search time 68.62 Seconds
(without alignments)
649.764 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLAIGCLYTLFTTFF.....DDGINSEWSKQWEGEDLS 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1184 | 63.2 | 383 | 11 | O88786 |
| 2 | 293.5 | 15.7 | 420 | 4 | Q14633 |
| 3 | 292.5 | 15.6 | 396 | 4 | Q14631 |
| 4 | 292 | 15.6 | 333 | 4 | Q15469 |
| 5 | 284.5 | 15.2 | 415 | 11 | Q920K4 |
| 6 | 260 | 13.9 | 349 | 6 | O97597 |
| 7 | 241.5 | 12.9 | 279 | 4 | Q9UDY5 |
| 8 | 190.5 | 10.2 | 363 | 13 | Q9DEQ1 |
| 9 | 170.5 | 9.1 | 881 | 13 | O57519 |
| 10 | 167 | 8.9 | 622 | 6 | Q9N0J7 |
| 11 | 165 | 8.8 | 296 | 6 | O18880 |
| 12 | 165 | 8.8 | 611 | 13 | Q9PTI0 |
| 13 | 165 | 8.8 | 611 | 13 | Q9IBF6 |
| 14 | 165 | 8.8 | 896 | 11 | O64146 |
| 15 | 159.5 | 8.5 | 890 | 11 | Q921A0 |
| 16 | 159 | 8.5 | 227 | 6 | Q9GLW3 |
| 17 | 157 | 8.4 | 581 | 6 | O46561 |
| 18 | 156 | 8.3 | 625 | 6 | Q9XS92 |
| 19 | 154.5 | 8.2 | 611 | 13 | Q9PTH9 |

20 151 8.1 206 4 Q16354
21 151 8.1 349 4 Q9UJ5
22 147.5 7.9 538 13 Q9DFU0
23 146.5 7.8 422 4 Q9UHS
24 145.5 7.8 422 4 O75462
25 144 7.7 217 6 O46386
26 143.5 7.7 425 11 Q9JM58
27 143.5 7.7 918 13 Q9W609
28 132 7.0 346 13 Q93404
29 130.5 7.0 198 6 O18985
30 130.5 7.0 390 4 Q9UEH7
31 126.5 6.8 329 4 Q9UQ41
32 117.5 6.3 896 4 Q13594
33 117.5 6.3 906 4 Q13593
34 117.5 6.3 958 4 Q13592
35 116.5 6.2 1282 5 Q9VWE0
36 114 6.1 371 4 Q9HC73
37 114 6.1 894 6 Q9MYL1
38 114 6.1 925 6 Q9MYK9
39 114 6.1 1163 6 Q9MYL2
40 114 6.1 1194 6 Q9MYL0
41 113.5 6.1 896 4 Q92919
42 113.5 6.1 958 4 Q92920
43 113.5 6.1 1165 4 Q92921
44 109.5 5.8 26926 4 Q10466
45 109 5.8 2221 5 Q9U1M1

ALIGNMENTS

RESULT 1
ID O88786 PRELIMINARY; PRT: 383 AA.
AC O88786;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IL-13 RECEPTOR ALPHA 2.
GN IL13RA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ; TISSUE=THYMUS;
RX MEDLINE=98391042; PubMed=9725226;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R.,
RA Collins M.;
RT "The murine IL-13 receptor alpha 2: molecular cloning,
characterization, and comparison with murine IL-13 receptor alpha 1.";
RL J. Immunol. 161:2317-2324(1998).
DR EMBL; U65747; AAC33240.1; -;
DR MGD; MGI:1277954; IL13ra2.
DR InterPro; IPR002996; -;
DR InterPro; IPR000532; -;
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 63.2%; Score 1184; DB 11; Length 383;
Best Local Similarity 64.0%; Pred. No. 9.2e-100;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

Oy 1 MAFVCLAIGCLYTLFTTSSSDTEIKVNPQDFEIVDPGVLYLYLQWQPLSLD 60
Db 1 MAFV--HRCCLCFLLCITGYS----LEIKVNPQDFEILDPLGLYLYLQWQPPVIE 54
Oy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLKNKIEAKITHLPMQCTNGSEVQ 120
Db 55 KFKGCTLEVLKYRNVDSNKTITIRNLKYKDGFDLKNKIEGKIRTHLSECTNGSEVQ 114

Query Match 15.7%; Score 293.5; DB 4; Length 420;
Best Local Similarity 28.1%; Pred. No. 1.2e-18;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

| | | | |
|----|-----|-----------------------------|-----|
| Qy | 309 | RSKNVIYCSDDGIWSEWSDKQCWEGD | 335 |
| Db | 309 | RAAVSSMCREAGLWSEWS-QPIVVGND | 334 |
| | | I : I : : : : | |

| | | | |
|----|-----|-----------------------------|-----|
| Db | 309 | RAAVSSMCREAGLWSEWS-QPIVVGND | 334 |
| | | I : I : : : : | |


```

RESULT      3
ID Q14631          PRELIMINARY;          PRT;    396 AA.
AC Q14631;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.
DS HSILSR2.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RX MEDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT Molecular cloning and expression of the human interleukin 5
RT receptor." ;
RL J. Exp. Med. 175:341-351(1992).
RM ENBL; X61177; CAA43484.1; -.
DR InterPro: IPRO02996; -.
DR InterPro: IPRO03532; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 21 396 INTERLEUKIN-5 RECEPTOR TYPE 2.
SQ SEQUENCE 396 AA; 44998 MW; 1AB60619842ACDA5 CRC64;
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Query Match 15.6%; Score 292.5; DB 4; Length 396;
Best Local Similarity 27.8%; Pred. No. 1.4e-18;
Matches 91; Conservative 58; Mismatches 143; Indels 35; Gaps

| | | | |
|----|-----|---|-----|
| Qy | 27 | DTIKVNPDPDFIVDGYLYLQWPPLSLDHFEKCEVTVELEYRNISETWKTIIT | 86 |
| Db | 25 | DEKISLLPPVFYIKVTG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYETRI | 82 |
| | | I : I : : : : : : : : : : : : : : | |
| Qy | 87 | KNLHYKGDFGLNGIEAKHTLELPWCNTSGEVSOSWAETTYWISPOGIPETKVQDMDCV | 146 |
| Db | 83 | ES---KCVTLHKGFSASVETLIQ----NHSLLASSWASAEHL-APPGPSGTISVNLTCT | 135 |
| | | : : : : : : : : : : : : : : : : | |
| Qy | 147 | -----YYNQYLL-CSWKPFGVLVDNTNYLFY----WYEGLDHALQCVDYIKAD | 191 |
| Db | 136 | TNTTNDYNSLRYSQVSLHCTVLGVTDPADETQFYLYRYGSWTE-----ECQEYSKDT | 189 |
| | | : : : : : : : : : : : : : : : : | |
| Qy | 192 | -QNIGICRRP-YLEASDYKDFYCINGSENKENPKIRSSFTFOLQVINVPPLPVLTFR | 248 |
| Db | 190 | LGRNIACWFPRTFILSKGRDWLAVLVYSGSKSHAIRPFOLFALHAIDAQINPLNVAEI | 249 |
| | | I : : : : : : : : : : : : : : : | |
| Qy | 249 | ESSECKLKSWIPLGPPIPARCFDYETIREDDTTLVATVENETYTLKTTNETROLFCVV | 308 |
| Db | 250 | EQT-RLSIQWEKPSAFPFHCFDYEVKIHNRNGYLQIEKLMTNAFISIIDLISKYDVQV | 308 |
| | | I : : : : : : : : : : : : : : : : | |

| | | | |
|----|-----|-----------------------------|-----|
| Qy | 309 | RSKNVIYCSDDGIWSEWSDKQCWEGD | 335 |
| Db | 309 | RAAVSSMCREAGLWSEWS-QPIVVGND | 334 |
| | | I : I : : : : | |

| | | | |
|----|-----|-----------------------------|-----|
| Db | 309 | RAAVSSMCREAGLWSEWS-QPIVVGND | 334 |
| | | I : I : : : : | |


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RESULT      4
ID Q15469          PRELIMINARY;          PRT;    333 AA.
AC Q15469;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
```

```
GN HSIL5R4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RX MEDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X62156; CAA44081.1; -.
DR InterPro; IPR002996; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal.
FT CHAIN 1 20
FT CHAIN 21 333
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 15.6%; Score 292; DB 4; Length 333;
Best Local Similarity 28.0%; Pred. No. 1.2e-18;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPQDPEIVDPGLVLYLOWQPPSLDHFKECTVEYELKYRNIGSETWKTIT 86
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
25 DEKISLLPVPNTIKVTG-LAQVLLQWPNPQEQ-RNVNLEYQVKINAKPEDDYEITR 82
QY 87 KNLHYKDFDLNKGIEAKIHTLLPQCTNGSEVQSWAETTYWISPOGIPETKVODMDCV 146
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
83 ES---KCVTLHKGSASVRIQLQ---NDHSLASWSAELH-APPGSPGTSVNLCT 135
QY 147 -----YNNWYLL-CSWKPGIGVLLDTNLYF-----WYGLDHALQCVDIYKAD 191
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 TMTEDNYSRLRSYQVSLHCTWGTAPEDQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPTRSSYFTFQLNIVKPLPPVYLTTR 248
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
190 LGRNACFPPTFTILSKGRDWLAVLVNGSSHSARLPDQFLHALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPICPARCFDYIEIREDDTTLVTATVENETTLKTTNETQLCFV 308
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
250 EGT-RLSIQWKPVSAPFHCFDYEVKIHNTENGVLQIEKLTNFAFISIDDLKSYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWS 326
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
309 RAAVSSMCREAGLWSEWS 326

RESULT 5
Q920K4 PRELIMINARY; PRT; 415 AA.
AC Q920K4;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.
GN GPIL-5RA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Norris T.E.;
RT "Cloning and Characterization of the Guinea Pig Interleukin-5 receptor
alpha cDNA.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U55215; AAD09361.1; -.
DR InterPro; IPR001777; -.

Query Match 13.9%; Score 260; DB 6; Length 349;
Best Local Similarity 25.7%; Pred. No. 1.1e-15;
Matches 78; Conservative 53; Mismatches 120; Indels 52; Gaps 14;
```

```
DR InterPro; IPR002996; -.
DR InterPro; IPR003532; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
DR SMART; SMO0060; FN3; 1.
KW Signal; Receptor.
FT CHAIN 1 17
FT CHAIN 18 415
SQ SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match 15.2%; Score 284.5; DB 11; Length 415;
Best Local Similarity 27.4%; Pred. No. 7.7e-18;
Matches 93; Conservative 55; Mismatches 149; Indels 43; Gaps 16;

QY 6 LAIGCLYFLISTTTCGCTSSSDTEIKVNPQDPEIVDPGLVLYLOWQPPSLDHFKEC 65
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7 ILLGAETLQTDTL-----PDKFLLPLPPIFTIKVTG-LAQVLLQWPNPQEQ-KNV 58
QY 66 TVEYELKYRNIGSETWKTITKNLHYKDFDLNKGIEAKIHTLLPQCTNGSEVQSWAE 125
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 NLNHYHKINTFOEEDYE---FRTQSKCETTLHOGVSASVRIIL-WH--GHSLLASSWS 112
QY 126 TTYWISPOGIPETKVODMDCV-----YNNWQ-----YLLCSWKPGIGVLLDTNLYF- 173
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
113 ABH-KAPPGSPGTSVNLCTTNTAASNYTNLKSVEVSLHCTWLAGKADAPEDQYFLYR 171
QY 174 ---WYGLDHALQCVDIYKAD-GQNGICRFP--YLEASDYKDFYICVNGSSSENKPTRSSY 227
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
172 YGPWTE-----ECQEYSKDTLSRNTACWFFPTFTFHSKARDRLAVHNGSSNHTIKPPD 225
QY 228 FTFQLNIVKPLPPVYLTFTRESSCEIKLWSIPLGPICPARCFDYIEIEI-REDDTTLVTA 286
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
226 QLFDTQADQPNPMDVTAETEGS-RLSIQWKPVSAPFHCFDYEVKICHTKDYQVEK 284
QY 287 TVENETYLKTTNETQLCFVYVRSKVNIVYCSDDGIWSEWS 326
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
285 TTNA--FVSTTDGVSKYSIQVRAAVSPHCRAMGLWSKWS 322

RESULT 6
Q97597 PRELIMINARY; PRT; 349 AA.
AC Q97597;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.L., Hirano A., Brown W.C., Estes D.M.;
RT "Biological activities of interleukin-13 on bovine lymphocytes:
implications for signaling through IL-13Ralpha.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF074402; AAC98147.1; -.
DR InterPro; IPR002996; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 13.9%; Score 260; DB 6; Length 349;
Best Local Similarity 25.7%; Pred. No. 1.1e-15;
Matches 78; Conservative 53; Mismatches 120; Indels 52; Gaps 14;
```

```
QY 53 WOPPLSLDHFKECTVEYELKYNIGSETWKTITITKNLHYKGFDLNKGIEAKIHTLLPWQ 112
Db 18 WNPPEGAS--PNCSLKY---FHFNGKQDKIAPET-HRSKEVPLNERICLQVGS---Q 67
QY 113 C-TNGSEVQSSWAETTYWISPOGIPETKVQDMDCVYVWQYLLCSWKFGIGVLLDTNVL 171
Db 68 CSTNESEKPSILVEKCF-SPPEGDPESAVALQCIWHNLRYMKCTWLPGRNASPDNPYIL 126
QY 172 FYWYEGDLHALQCVDIKADGONICRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFT 229
Db 127 YVWHSNLKILQCENFYR-EGOHIACSNLRKVKDSSFQHSQVQVWVRDNRAGKISPSFNI 185
QY 230 FOLQNVKPLPVYLTFTRESCEIKLWSPGLPIPARCFDYEIEIREDDTTLVATVRE 289
Db 186 VPLTSHVAP-DPSHIKLSFQNGDLVQWNTPNQ-FQSQCLCYEVEVINSHA----- 235
QY 290 NETYTLTKTNETR-----QLCFV-----RSKNVNYC-SDDGIWS 323
Db 236 -ETHDIFYVEAKONTEFEGNLECTICFMVPGVLPDLTNTVIRIRVKTNKLCEYEDDKLWS 294
QY 324 EWS 326
Db 295 NWS 297
```

RESULT 7

```
Q9UDY5 PRELIMINARY; PRT; 279 AA.
AC Q9UDY5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE INTERLUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U01380; A000511.2; -
DR HSSP; P40189; IBOU.
DR InterPro; IPR002996; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;
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Query Match 12.9%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 3.9e-14;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;
QY 11 LYTFLLSTFTGCTSSDTEIKVNPQDFEIVDPGLYLYLQWOPPLSLDHFKECTVEY- 69
Db 10 LWALLCAGGGGGGGAAPTETQPPVTNLVSVENLCTVITWNPPEGAS--SNCSLWYF 67
QY 70 ----ELKRYNTGSETWKTITITKNLHYKGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124
Db 68 SHFGDKQDKKIAPETRRSI-----EVLPLNERICLQVGS---QSTNESEKPSILV 114
QY 125 ETTYWIS-POGIPETKVQDMDCVYVWQYLLCSWKFGVLLDTNLYWYEGDLHALQ 183
Db 115 EKC--ISPEGDPESAVALQCIWHNLRYMKCTWLPGRNASPDNPYILYVWHSLEKITHQ 172
QY 184 CVDYIKADQNGICRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFTFQNLQVTKPLPP 241
Db 173 C-ENIFREGQVFGCSFDLTVKDSSFEQHSQVQVWVRDNRAGKISFNIPLVTSRKVPDP 231
QY 242 --VYLTFRESCEIKLWSPGLPIPARCFDYEIEIREDDT 281
Db 232 HIKNLSFHD---DLYQVQWNPQNF1-SRCLFYEVVNNSTQ 269
```

RESULT 8

```
Q9DEQ1 PRELIMINARY; PRT; 363 AA.
AC Q9DEQ1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T., Secombes C.J.;
RT "Cloning and expression of the first non-mammalian cytokine receptor
RT common gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1; -
KW Receptor.
FT NON_TER
SQ SEQUENCE 363 AA; 41861 MW; DF69B2EE3EEA06D3 CRC64;
```

```
Query Match 10.2%; Score 190.5; DB 13; Length 363;
Best Local Similarity 22.9%; Pred. No. 2.4e-09;
Matches 55; Conservative 48; Mismatches 118; Indels 19; Gaps 6;
```

```
QY 97 LNKGEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVYVWQYLLCS 156
Db 1 IHKVYRVELVTLPIVTHFDMKMGWSW--LELLISLQGYEAPTPNVNCLINDYVNCI 58
QY 157 WKPGIGVLLDTNLYWYEGDLHALQCVDIKADGQNGICRFPYLEASDYKDFYICVNG 216
Db 59 WSE--QSIPEVNTFFSSRFKDNMEECTYLOEESYAVGCRSLYDKSDRFR----- 108
QY 217 SSENKPIRSSYFTFQ---LQNVKPLPVYLTFTRESCEIKLWSPGLPIPARCFDYE 273
Db 109 TLKTKLVHQNNYSYVQDHNLSKMKVLYPPVNLSEVMKNKDPENLYWNNSKNFTF---CIESE 165
QY 274 IEIREDDTTLVTATVENE-TYTLKTTNETROLCFVRSKVNLYCGDDGIWSEWSKQWCE 332
Db 166 VYRINSKWKTSFSPKEQKYAVAFPLKSSRYEQVQVAVNDMCGESEFSEWSQIOWD 225
```

RESULT 9

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Q57519 PRELIMINARY; PRT; 881 AA.
AC Q57519
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GP130P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -
DR HSSP; P40189; IBOU.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003529; -
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
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QY 251 SCBK-----LKWSIP-LGPIPARCF--YEIEIREDDTTLVTATVENEYTLTKT 299
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 135 -VEVQPEDKKPYLWIKWSPPTLIDLKGTWFTLLYEQLKPENAE-----EWETHFAQ 187

QY 298 TNETRQLCFVRSK--VNIIYS-DDGIWSEWS 326
   : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 188 QTFKVLSLHGGOKYLVQVRCKPDHGYWSSWS 219

RESULT 11
ID O18880 PRELIMINARY; PRT; 296 AA.
AC O18880;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97375450; PubMed=9231767;
RT Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RL tissues.";
RL Endocrinology 138:3187-3194(1997).
DR EMBL; AF027403; AAB83999.1; -.
DR HSSP; P14787; IAN3.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003528; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
DR SEQUENCE 296 AA; 33854 MW; 9F1C15FB41DE0787 CRC64;

Query Match 8.8%; Score 165; DB 6; Length 296;
Best Local Similarity 31.3%; Pred. No. 3.8e-07;
Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps

QY 136 PETKVOQDMCVYVNWYLLCSNKPGGIGVLIDTNLYFYWYEGLDHALQCVDYIKADQNI 195
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 27 PPEKPLVKCRSPCKETFTCWPEAGDGLPTNYLYHKEGELTHECPDY-KTGGPN- 84

QY 196 GCRFPYLEADYKDFICVNGSENKPIRSYFTFQNLQNVKPLPVYLTFTRESSCEIK 255
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 85 SCYFSKKHTSIWKMYITVNAIQMGITSSSDPLVHVHTYIPEPPANLTLLELKHPEDR 144

QY 256 ----LKWSIP-LGPIPARCF--DYEIEIREDDTTLVTATVENEYTLTKTN-ETRQLCF 306
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 145 PYLWIKWSPPTMTDVKSGVFIIQYIIRLKEPKAT-----DWETHFTLQTLKIFNLYP 198

QY 307 VRSKVNIIYS-DDGIWSEWS 326
   : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 199 GQKYLQVRCKPDHGYWSSWS 219

RESULT 12
Q9PTIO PRELIMINARY; PRT; 611 AA.
ID Q9PTIO
AC Q9PTIO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.

```

```
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.D.;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL: AF193800; AAF05776.1; -
DR HSP: P16471; Ibp3
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match 8.8%; Score 165; DB 13; Length 611;
Best Local Similarity 28.0%; Pred. No. 9.5e-07;
Matches 61; Conservative 28; Mismatches 91; Indels 38; Gaps 10;

QY 127 TYWISPGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYVYEGLDHALQCV 186
D 127 TYWISPGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYVYEGLDHALQCV 186
D 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGSGDGLPTNYSLLYRKENDPKIYEC 80
D 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGSGDGLPTNYSLLYRKENDPKIYEC 80
QY 187 YKADGQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQINVK 239
D 187 YKADGQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQINVK 239
D 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGNSVNSDESDVTY-----IVQ 131
D 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGNSVNSDESDVTY-----IVQ 131
QY 240 PPVLTFTRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIRDDTTLVTAT 289
D 240 PPVLTFTRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIRDDTTLVTAT 289
D 132 PPTNVS LAVESGHDLKWK-----LPPAMVDVQSGWLTILKYVRYKEKEQWEAHL 185
D 132 PPTNVS LAVESGHDLKWK-----LPPAMVDVQSGWLTILKYVRYKEKEQWEAHL 185
QY 290 NETYLTKTNETRQLCFVVRSKVNIYCS-DDGIWSEWS 326
D 290 NETYLTKTNETRQLCFVVRSKVNIYCS-DDGIWSEWS 326
D 186 GNQLKLFGLTPGNGYVQ-----VRCRPSDGHSEWS 219
D 186 GNQLKLFGLTPGNGYVQ-----VRCRPSDGHSEWS 219

RESULT 14
Q64146
ID Q64146 PRELIMINARY; PRT; 896 AA.
AC Q64146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3K<BETA>.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appling K., Butini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo.";
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: S79263; AAB35068.1; -
DR EMBL: AJ000555; CAA04186.1; -
DR InterPro; IPR000282; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam: PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT NON_TER 1
FT NON_TER 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match 8.8%; Score 165; DB 11; Length 896;
Best Local Similarity 20.5%; Pred. No. 1.5e-06;
Matches 77; Conservative 62; Mismatches 156; Indels 80; Gaps 18;

QY 5 CLATIGCL--YT-FLISITTFGCTSSSDTEIKVN-----PPQDFEIVDPCGLCYL 49
D 5 CLATIGCL--YT-FLISITTFGCTSSSDTEIKVN-----PPQDFEIVDPCGLCYL 49
D 94 CVPRRCVLPYTFQFSVKEDYISLQPDROLSIHLVPLAQHVQPPPKDISISPSG--DHF 151
D 94 CVPRRCVLPYTFQFSVKEDYISLQPDROLSIHLVPLAQHVQPPPKDISISPSG--DHF 151
QY 50 YLQWQPPPL---SLDHFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNKGTEAKI 106
D 50 YLQWQPPPL---SLDHFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNKGTEAKI 106
D 152 LLKWSVPLGDAQVSLLSOKDIOFEVAYKQL-QDSWED--ASSLH-----TCNLWVLEPK 203
D 152 LLKWSVPLGDAQVSLLSOKDIOFEVAYKQL-QDSWED--ASSLH-----TCNLWVLEPK 203
QY 107 TLLP-----WQCTNGSEVQ---SSAETTWISQGIPETKVQDMDCVYNNQYLL 154
D 107 TLLP-----WQCTNGSEVQ---SSAETTWISQGIPETKVQDMDCVYNNQYLL 154
D 107 TLLP-----WQCTNGSEVQ---SSAETTWISQGIPETKVQDMDCVYNNQYLL 154
```

```
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.D.;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL: AF193800; AAF05776.1; -
DR HSP: P16471; Ibp3
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match 8.8%; Score 165; DB 13; Length 611;
Best Local Similarity 28.0%; Pred. No. 9.5e-07;
Matches 61; Conservative 28; Mismatches 91; Indels 38; Gaps 10;

QY 127 TYWISPGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYVYEGLDHALQCV 186
D 127 TYWISPGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYVYEGLDHALQCV 186
D 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGSGDGLPTNYSLLYRKENDPKIYEC 80
D 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGSGDGLPTNYSLLYRKENDPKIYEC 80
QY 187 YKADGQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQINVK 239
D 187 YKADGQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQINVK 239
D 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGNSVNSDESDVTY-----IVQ 131
D 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGNSVNSDESDVTY-----IVQ 131
QY 240 PPVLTFTRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIRDDTTLVTAT 289
D 240 PPVLTFTRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIRDDTTLVTAT 289
D 132 PPTNVS LAVESGHDLKWK-----LPPAMVDVQSGWLTILKYVRYKEKEQWEAHL 185
D 132 PPTNVS LAVESGHDLKWK-----LPPAMVDVQSGWLTILKYVRYKEKEQWEAHL 185
QY 290 NETYLTKTNETRQLCFVVRSKVNIYCS-DDGIWSEWS 326
D 290 NETYLTKTNETRQLCFVVRSKVNIYCS-DDGIWSEWS 326
D 186 GNQLKLFGLTPGNGYVQ-----VRCRPSDGHSEWS 219
D 186 GNQLKLFGLTPGNGYVQ-----VRCRPSDGHSEWS 219

RESULT 13
Q9IBF6
ID Q9IBF6 PRELIMINARY; PRT; 611 AA.
AC Q9IBF6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
RT "Cloning of a cDNA for Xenopus prolactin receptor and its
RT metamorphic expression profile.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB030443; BAA30400.1; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

Query Match 8.8%; Score 165; DB 13; Length 611;
Best Local Similarity 28.0%; Pred. No. 9.5e-07;
```

| | | | |
|----|-----|--|-----|
| Db | 204 | LFLPNSIVVARVRAQLAPGSSLSGRSGWSPEVHWDSPTB-DKARPQNQLCPFDGIGTQSLN | 262 |
| Qy | 155 | CSWKPGIGVLLDTNYNLFYWYEGLDHALQCDYIKADGQGNIGRCRFPYLEASDYKDFYICV | 214 |
| Db | 263 | CSWEVTKVTDVSFGLFYSYSSPKAGEKKSPVKE-----LQASRYTRVHCSL | 311 |
| Qy | 215 | NGSSENKPIRSSVFTFQLO-----NIVKPLPP-VYLFTFRESSEIKLKSIDL | 262 |
| Db | 312 | NVSD---PAAHSQTVSVKRLGCKFTIESFNHIOAMPPTLNTLNKRDSD---YSLHWETOK | 365 |
| Qy | 263 | GPIPARCFDYEIER-----EDDTTLVTATVENEYVTLKTTNETQLCFVVRKSNVNYC | 316 |
| Db | 366 | MSYPFFIQHAFQVQYKKKLDRWEDSKT-----ENLNHAHSMDLPOLEFGTSYCARVRVKTIP | 421 |
| Qy | 317 | SDDGINSEWSDKQCV | 331 |
| Db | 422 | EYKGLWSEWSNCTW | 436 |

RESULT 15

| | |
|--------|--|
| RESULT | 15 |
| Q9Z1A0 | |
| ID | Q9Z1A0 PRELIMINARY; PRT; 890 AA. |
| AC | Q9Z1A0; |
| DT | 01-MAY-1999 (TtEMBLrel. 10, Created) |
| DT | 01-MAY-1999 (TtEMBLrel. 10, Last sequence update) |
| DE | 01-MAR-2001 (TtEMBLrel. 16, Last annotation update) |
| DE | INTERLEUKIN-5 RECEPTOR BETA CHAIN. |
| GN | IL5. |
| OS | Eukia porcellus (Guinea pig). |
| OC | Caviaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia. |
| OX | NCBI_TaxID=10141; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RA | Logsdon N.J., Graham A., Scott C.W.; |
| RA | "Guinea pig IL5 receptor beta chain."; |
| RL | Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases. |
| RL | EMBL; U94688; AAC77520.1; -. |
| DR | InterPro; IPR000276; -. |
| DR | InterPro; IPR001777; -. |
| DR | InterPro; IPR002996; -. |
| DR | InterPro; IPR003531; -. |
| DR | Pfam; PF00041; fn3; 3. |
| DR | PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1. |
| DR | PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1. |
| DR | SMART; SM00060; FN3; 1. |
| KW | Receptor. |
| SQ | SEQUENCE 890 AA; 96578 MW; D43FB1CA88525536 CRC64; |

```

Query Match      8.5%; Score 159.5; DB 11; Length 890;
Best Local Similarity 24.1%; Pred. No. 4.8e-06;
Matches 81; Conservative 47; Mismatches 135; Indels 73; Gaps 19;

QY 34 PPQDFEIVDPCGYLYLQWQPPLSLDH---FKECTVEYELKRYNIGSETWKTITIKMLH 90
    |||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 138 PPQDVQINTSG---DOVLLTWSVALLEGPHTSWLSQRDLEFEVVYKRL-HEPWESAST--LH 192
    |||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 91 YKDG-----FDLNKGLIEAKIHTLLPWQCTNGSEVQ---SSNAETTYWLSPOGIPETK 139
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 193 SNSSQAALGPELFLPSTTYVARVTRT-----ARGSGFSGRFSQWSPVSSQGP-DQAQ 247
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 140 VQDMDCVYYNQQYLLCSWPKPGIGVLLDTNTNLFYWGELDHALQ-CVDYIKADGONI--- 195
    || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 248 PQNLQCVFDGAHTLSCSWEVRSQVTSVSGFLFY-RSLDAGEQCCQVQKEELHDIVTR 306
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 196 -GCRFPYLEASDYKDFICYNGSSSENKPISTYFFQLQNIKVLPPVYLFTFTRESSCEI 254
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 307 HSCQIRVSNRPHSQYTVTVPRNGEAFIRSA-----NHIQMAAPT-LNVTKDGD-TY 357
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 255 KLKWSIPLGPTPARCF-----DYEIEIREDDTLTVATVENEYTYLK----- 296
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 358 SLRW-----VTEKMYXSHIENTEIQVR-----FAGDQWENSKTETLKNAHMPPLPLEP 407
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:54 ; Search time 43.66 Seconds
(without alignments)
598.440 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901

Sequence: 1 MAFVCLAIGCLYFLISTTF.....EWSRQCWGEDLSRKTLRL 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 294.5 | 15.5 | 420 | 2 S21052 | interleukin-5 rece |
| 2 | 292 | 15.4 | 335 | 2 A40267 | interleukin-5 rece |
| 3 | 254 | 13.4 | 831 | 2 JQ1655 | prolactin receptor |
| 4 | 229 | 12.0 | 415 | 2 S12357 | interleukin-5 rece |
| 5 | 210.5 | 11.1 | 830 | 2 I50455 | prolactin receptor |
| 6 | 208 | 10.9 | 369 | 2 A42365 | interleukin-2 rece |
| 7 | 206 | 10.8 | 373 | 2 A55718 | interleukin-2 rece |
| 8 | 198.5 | 10.4 | 369 | 2 I49280 | interleukin-2 rece |
| 9 | 179 | 9.4 | 878 | 1 A40091 | prolactin receptor |
| 10 | 165 | 8.7 | 310 | 2 A29884 | prolactin receptor |
| 11 | 165 | 8.7 | 412 | 2 A41070 | prolactin receptor |
| 12 | 165 | 8.7 | 581 | 2 I45971 | prolactin receptor |
| 13 | 165 | 8.7 | 610 | 2 A34631 | lactogen receptor |
| 14 | 165 | 8.7 | 610 | 2 A36116 | prolactin receptor |
| 15 | 165 | 8.7 | 896 | 2 I56363 | interleukin-3 rece |
| 16 | 160 | 8.4 | 897 | 1 A39255 | cytokine receptor |
| 17 | 159 | 8.4 | 292 | 2 I77525 | prolactin receptor |
| 18 | 159 | 8.4 | 303 | 2 I77524 | prolactin receptor |
| 19 | 159 | 8.4 | 608 | 2 I53269 | cytokine receptor |
| 20 | 155.5 | 8.2 | 896 | 1 A35782 | prolactin receptor |
| 21 | 151 | 7.9 | 622 | 2 A40144 | prolactin receptor |
| 22 | 150.5 | 7.9 | 917 | 2 I49699 | glycoprotein 130 - |
| 23 | 147 | 7.7 | 616 | 2 A30304 | prolactin receptor |
| 24 | 133.5 | 7.0 | 333 | 2 S13684 | granulocyte-macrop |
| 25 | 133.5 | 7.0 | 378 | 2 S50040 | granulocyte-macrop |
| 26 | 133.5 | 7.0 | 400 | 2 S06945 | granulocyte-macrop |
| 27 | 130.5 | 6.9 | 378 | 2 A40266 | interleukin-3 rece |
| 28 | 129 | 6.8 | 150 | 2 B34631 | lactogen receptor |
| 29 | 128 | 6.7 | 630 | 2 I51086 | prolactin receptor |

30 126.5 6.7 918 2 A36337 membrane glycoprot
31 123.5 6.5 1097 2 S17308 leukemia inhibitor
32 122.5 6.4 286 2 S50039 granulocyte-macrop
33 112.5 5.9 1630 2 C41214 protein-tyrosine-p
34 111.5 5.9 1557 2 D41214 protein-tyrosine-p
35 109.5 5.8 918 2 A44257 interleukin-6 sign
36 109.5 5.8 26926 1 I38344 titin - rabbit (fir
37 106.5 5.6 6805 2 S20901 titin - cardiac mus
38 106 5.6 634 2 S33339 somatotropin recep
39 105.5 5.5 1825 2 T32828 hypothetical prote
40 105 5.5 837 2 A34898 granulocyte colony
41 104 5.5 771 2 B38252 granulocyte colony
42 104 5.5 783 2 JH0329 granulocyte colony
43 104 5.5 863 2 C38252 granulocyte colony
44 100 5.3 817 2 A48721 titin, muscle - ch
45 99.5 5.2 638 2 S12136 somatotropin recep

ALIGNMENTS

RESULT 1

S21052

Interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence.revision 10-Nov-1995 #text_change 01-Dec-2000
C:Accession: S21052; S21053; A46175; S78106; S78107
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992

A:Title: Molecular cloning and expression of the human interleukin 5 receptor.

A:Reference number: S21050; MUID:92121815

A:Accession: S21052

A:Molecule type: DNA

A:Residues: 1-420 <MUR>

A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844

A:Experimental source: clone lambda h5R.12

A:Accession: S21050

A:Molecule type: DNA

A:Residues: 1-395, 'I', <MU2>

A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

A:Experimental source: clone lambda h5R.27

A:Accession: S21053

A:Molecule type: mRNA

A:Residues: 1-332, 'K', <MU3>

A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

A:Experimental source: clone lambda h5R.25

R:Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992

A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum

A:Reference number: A46175; MUID:92357767

A:Accession: A46175

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 333-420 <TAV>

A:Experimental source: HL-60 cells and eosinophils

A:Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIF:116244)

R:Murata, Y.

submitted to the EMBL Data Library, July 1991

A:Reference number: S78106

A:Accession: S78106

A:Molecule type: DNA

A:Residues: 1-128, 'I', 130-395, 'I', <MUW>

A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

R:Murata, Y.

submitted to the EMBL Data Library, September 1991

A:Reference number: S78107

A:Accession: S78107

A:Molecule type: mRNA

A:Residues: 1-128, 'I', 130-332, 'K', <MU4>

A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

F;345-365/Domain: transmembrane #status predicted <TM>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.5%; Score 294.5; DB 2; Length 420;
Best Local Similarity 28.2%; Pred. No. 4.2e-16;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

```
QY 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPSLDHFKECTVEYELKYNIGSETWKIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPPVNFITIKVGT-LAQVLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKGFDLNKGIEKIHTLWPQCTNGSEVOSSWAETTYISPOGIPETKVDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APGSPGTSVNLNCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YYNQYLL-CSWKPGIGVLDTNLYFY----WYEGLDHALQCVDIYKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTETDNYSLRSLQVSLHCTWLVGTDAEDTQFLVRYGSWTE-----ECQEYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVLTFR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPTFTILSKGRDLWLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWISPLGPIPARCFDYEIREDDTTLVTATVENETYLTKTNETRQLCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 EGT-RLSTQWEKPVSAPIHCFDYEVIHNTNRNGYLQIEKLTNAFISIDDLKSYDVQV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 RSKVNIYCSDGDIWSEWSKOCWEGEDLSK 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337
```

RESULT 2
A:040267
Interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuytens, T.; Van der Heyden, J.; Fiers, W.; Pl
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <FAV>
A:Cross-references: GB:W75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 15.4%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 5e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

```
QY 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPSLDHFKECTVEYELKYNIGSETWKIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPPVNFITIKVGT-LAQVLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKGFDLNKGIEKIHTLWPQCTNGSEVOSSWAETTYISPOGIPETKVDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APGSPGTSVNLNCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YYNQYLL-CSWKPGIGVLDTNLYFY----WYEGLDHALQCVDIYKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTETDNYSLRSLQVSLHCTWLVGTDAEDTQFLVRYGSWTE-----ECQEYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVLTFR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPTFTILSKGRDLWLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWISPLGPIPARCFDYEIREDDTTLVTATVENETYLTKTNETRQLCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Db 250 EGT-RLSTQWEKPVSAPIHCFDYEVIHNTNRNGYLQIEKLTNAFISIDDLKSYDVQV 308
QY 309 RSKVNIYCSDGDIWSEWS 326
 :
Db 309 RAAVSSMCREAGLWSEWS 326
 :
RESULT 3
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: kidney
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 13.4%; Score 254; DB 2; Length 831;
Best Local Similarity 27.3%; Pred. No. 1.8e-12;
Matches 93; Conservative 48; Mismatches 158; Indels 42; Gaps 14;
QY 18 TTFCTSSSTEIKVN--PPQDFE---IVDPG-----YLGILYLQWQPPSL 59
 :
Db 97 TTFNITVATNEIGSNSDDQYVDVTISVQPGSPVNLTKRSANIMYLWAKSPPLLA 156
 :
QY 60 DHFKECTVEYELKYNIGSETWKIITIKNLHYKDFGLNKGIEAKIHTLLPWQCTNGSEV 119
 :
Db 157 DASSNHLHYELRIKPEKEWETI---SVGVTQCKINR-LNAGMRVYVQVRCVLTDPGE 212
 :
QY 120 QSSWAETTYNISPOG-IPETKVDQMDCVYINWOYLLCSWKPGIGVLDTNLYFWVEGL 178
 :
Db 213 WSESSERHLIPSGQSPPEKPTTIKRSPEKETFTCWKPKGLDGGHPTNTLLYSKEGE 272
 :
QY 179 DHALQCVDIYKADQNLGICRFPYILEASDYKDFYICVNGSSSENKPIRSYFTFQNLQIVKP 238
 :
Db 273 EQVYECPDY-RTAGPN-SCYFDKKHTSFYIYINIVTRATNEMSGNSDDPHYVDVYIIVQ 330
 :
QY 239 LPVYLFTTRESSCEIK-----LKWS-IPLPARPACRDEYIEIR---EDDTTLTAVTEN 290
 :
Db 331 DPPNVVTLKLPKINRKPVLVLTWSPPLADVRSGWLTLEYELRKPEGEWETIFVQ 390
 :
QY 291 ET-YLTKTTETQLCFVVRSKVNIYCSDD--GIWSEMSDK 328
 :
Db 391 QTYKMFSLNPGPKYI-----IQIHCCKPDHHSWSEWS 425
 :

RESULT 4
S12357
interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S12357
R:Takaki, S.; Tomimaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu
EMBO J. 9, 4367-4374, 1990
A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; MUID:91092260
A:Accession: S12357
A:Status: preliminary

Db 181 HCLEHLVQYRFDWDHSTEQSDVYRHKFLSPVDGQKRYTRVRKSRFNPLCGSAQHSEW 240
 Qy 326 SDKOCWEGEDLSKK 339
 Db 241 SHPIHW-GSNTSKE 253
 RESULT 7
 A55718
 interleukin-2 receptor gamma chain precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
 C:Accession: A55718
 R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg, F.
 Genomics 23, 69-74, 1994
 A:Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combined
 A:Reference number: A55718; MUID:95130114
 A:Accession: A55718
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-373 <HEN>
 A:Cross-references: GB:U04361; NID:g517411; PIDN:AAAC48403.1; PID:g517412
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication
 Query Match 10.8%; Score 206; DB 2; Length 373;
 Best Local Similarity 27.3%; Pred. No. 4.5e-09;
 Matches 67; Conservative 42; Mismatches 100; Indels 36; Gaps 11;
 Qy 115 NGSE-----VSSWAETTYWISPOGIPETKYQDMDCVYINMYQLCSW-----KPGI 161
 Db 31 NGNEDITPDEFLLATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSEPRP-- 82
 Qy 162 GVLLDTYNLFYWEGL--DHALQCVDYIKADGQNTGCRFPYLEASDYKDFYICVNGSSE 219
 Db 83 -----TNLTTHYKNSNDKDVQECGHYLFSEVTAGCWLQKEEIHLYETFFVQLRDPRE 137
 Qy 220 NKPIRSYFTFQLQNIKVPPLPVVLTFTRESSCEIKLKWISPLGPIPARCFDYEIETRED 279
 Db 138 --PRQSTQKLQNLVYPAPENLTLLHNSQLSELSWS---NRHLDCLEHVQVRSR 192
 Qy 280 -DTLVATVTVN-ETYLTKTNTETRLQLCFVVRKVNITYCSDDGINSWSDKOCWEGEDLS 337
 Db 193 WDRSWTEQSDVHRNSFSLSPVDGQKRYTRVRKSRFNPLCGSAQRWSEWSHPHW-GSNTS 251
 Qy 338 KKTLL 342
 Db 252 KENPL 256
 RESULT 8
 I49280
 interleukin-2 receptor gamma chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
 R:Cao, X.; Kozak, C.A.; Liu, Y.
 Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
 A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) ga
 A:Reference number: A47514; MUID:93391374
 A:Accession: I49280
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <CAO>
 A:Cross-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350
 A:Accession: A47514
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-369 <RE2>
 A:Cross-references: GB:I20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.

Biochem. Biophys. Res. Commun. 193, 356-363, 1993

A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of functional expression of the recombinant protein in T cells

A:Reference number: JN0592; MUID:93277575

A:Accession: JN0592

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-369 <K0M>

A:Cross-references: DDBJ:D13355; NID:g303684; PIDN:BAA02760.1; PID:g303685

R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T. Gene 130, 303-304, 1993

A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma chain

A:Reference number: JN0775; MUID:93366191

A:Accession: JN0775

A:Molecule type: mRNA

A:Residues: 1-369 <K0B>

A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046

R:Chiu, R.K.; Dougherty, G.J. submitted to the EMBL Data Library, October 1993

A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain

A:Reference number: S37582

A:Accession: S37582

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>

A:Cross-references: EMBL:X75337

R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Eur. J. Immunol. 24, 3014-3018, 1994

A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal location, and expression

A:Reference number: I53398; MUID:95104285

A:Accession: I53398

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555

C:Genetics:

A:Gene: IL-2Rgamma

A:Introns: 39/1, 90/2; 152/1; 199/3; 254/1; 286/2; 308/3

C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHS2), beta and gamma chains

C:Function:

A:Description: receptor for interleukin-2

A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N cells

C:Superfamily: interleukin-2 receptor gamma chain

C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein

F:1-2/Domain: signal sequence #status predicted <SIG>

F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>

F:256-284/Domain: transmembrane #status predicted <TMW>

F:71,75,84,196,159,164,306/Binding site: carbohydrate (Asn) #status predicted <TMM>

| | | | | |
|-----------------------|--------|--|---------------------------------|-------------|
| Query Match | 10.4%; | Score 198.5; | DB 2; | Length 369; |
| Best Local Similarity | 26.5%; | Pred. No. 1.8e-08; | | |
| Matches | 54; | Conservative 38; | Mismatches 95; | Indels 17; |
| Gaps | | | | |
| Qy | 136 | PETKQVDMDCVYNNQYLLCSW---- | KPGIGVLLDTNNLIFYWYEGLDHAL-- | QCVDYIK 189 |
| | | : :: : : : : | : : : : : : | |
| Db | 53 | PTLPLPEVQCVEFNIEYMNCTWSSSPPQA----- | TNLTLYHYRYKVSDNNNTFOECSHYLF | 107 |
| Qy | 190 | ADGONICRCRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLOINIVKLPVPVYLLFTRE | 249 | |
| | | : :: : : : : | : :: : : : : | |
| Db | 108 | SKETSCGCIQEKEDIQYQTFVVOL-- | ODPKQPORRAVQKLNQINVIPRAPENLTSLN | 165 |
| Qy | 250 | SSCIEIKLWSIPLGPIPARCFDVEIEIRED-DTTLVTATVENE-TYTLKTTNTETROLCFV | 307 | |
| | | : :: : : : : | : : : : : : | |
| Db | 166 | SESQLELRWK--SRHIKERCILYQVRSNRDRKSWTELIVNHHPREFSLPSVDKLKRYTFR | 223 | |
| Qy | 308 | VRSKVNIYCSDDGIWSEWSDKQCW | 331 | |
| | | : : : : : | : : : : : | |
| Db | 224 | VRSYRNPICGSSQQWKSQPVHW | 247 | |
| RESULT | 9 | | | |
| A40091 | | | | |

Db 130 LEVQKLDKKTLYLWVWSPPTITDVKGTWFTMEYR-----LKPEAEWEIHTFGH 182
QY 301 TRQL-----CFVVRSKVNIYCSDDGIWSEWSKQWE 332
Db 183 QTQFKVFDLYPGQKYLVTQTRCK---PDHGYWSRWSQESSVE 220
RESULT 12
145971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>
Query Match 8.7%; Score 165; DB 2; Length 581;
Best Local Similarity 31.3%; Pred. No. 1.5e-05;
Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;
QY 136 PETRVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYWYEGLDHALQCVDIKADQNI 195
Db 27 PPERKPLVKCRSPGKETFTCWNPCTDGLTPTNYSLTYSKEGETTYECPDY-KTGGPN- 84
QY 196 GCRPPYLEASDYKDFYICVNGSSNKPISYFTFQLNIVKPLPPVYLFTTRESCEIK 255
Db 85 SCYFSKKTHTSIWKVYITVNAINGISSDPLVHVHYIIVEPEPPANLTLELKHPEDRK 144
QY 256 ----LKWSSIP-LGPIPARCF--DYEIREDDTTLVATVENET-YILKTN-ETROLCF 306
Db 145 PYLWIKSPPTMTDVKGWFIQRIEKLKPEKAT-----DWETHFTLKQTLKFIENLYP 198
QY 307 VVRSKVNIYCS-DDGIWSEWS 326
Db 199 GQKYLQIRCKPDHGYSEWS 219
RESULT 13
A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 28-Jul-2000
C:Accession: A34631
R:Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A:Reference number: A34631; MUID:90241201
A:Accession: A34631
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <ZHA>
A:Cross-references: GB:M34083; NID:g205122; PIDN:AAA79273.1; PID:g205123
A:Note: the authors translated the codon GAG for residue 533 as Gly
C:Superfamily: cytokine receptor homology
F:31-216/Domain: cytokine receptor homology <CRS>
Query Match 8.7%; Score 165; DB 2; Length 610;
Best Local Similarity 28.5%; Pred. No. 1.6e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

QY 131 SPOGIPETKVDMDCVYNNQYLLCSWKPGIGVLLDTNLYWYEGLDHALQCVDIKA 190
Db 21 SPFGKPEIH-----KCRSPDKETFTCWNPCTDGLTPTNYSLTYSKEGETTYECPDY-KT 75
QY 191 DQONIGCRPPYLEASDYKDFYICVN-----GSSENKPIRSYFTFQLNIVKPLPPVYL 245
Db 76 SGNP-SCFFSKQYTSIWKYIITVNATNMGSSSDPL-----YVDVYIIVEPEPPRNL 129
QY 246 F---TRESSCEIKLWSSIP-LGPIPARCFDYEIREDDTTLVATVENETYLTKTNE 300
Db 130 LEVQKLDKKTLYLWVWSPPTITDVKGTWFTMEYR-----LKPEAEWEIHTFGH 182
QY 301 TRQL-----CFVVRSKVNIYCSDDGIWSEWSKQWE 332
Db 183 QTQFKVFDLYPGQKYLVTQTRCK---PDHGYWSRWSQESSVE 220
RESULT 14
A36116
prolactin receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 28-Jul-2000
C:Accession: A36116
R:Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, M.; Endocrinol. 4, 1136-1143, 1990
A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A:Reference number: A36116; MUID:91155946
A:Accession: A36116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <SHI>
A:Cross-references: GB:M57668; NID:g206366; PIDN:AAA41938.1; PID:g206367; GB:M60728
C:Superfamily: cytokine receptor homology
F:31-216/Domain: cytokine receptor homology <CRS>
Query Match 8.7%; Score 165; DB 2; Length 610;
Best Local Similarity 28.5%; Pred. No. 1.6e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;
QY 131 SPOGIPETKVDMDCVYNNQYLLCSWKPGIGVLLDTNLYWYEGLDHALQCVDIKA 190
Db 21 SPFGKPEIH-----KCRSPDKETFTCWNPCTDGLTPTNYSLTYSKEGETTYECPDY-KT 75
QY 191 DQONIGCRPPYLEASDYKDFYICVN-----GSSENKPIRSYFTFQLNIVKPLPPVYL 245
Db 76 SGNP-SCFFSKQYTSIWKYIITVNATNMGSSSDPL-----YVDVYIIVEPEPPRNL 129
QY 246 F---TRESSCEIKLWSSIP-LGPIPARCFDYEIREDDTTLVATVENETYLTKTNE 300
Db 130 LEVQKLDKKTLYLWVWSPPTITDVKGTWFTMEYR-----LKPEAEWEIHTFGH 182
QY 301 TRQL-----CFVVRSKVNIYCSDDGIWSEWSKQWE 332
Db 183 QTQFKVFDLYPGQKYLVTQTRCK---PDHGYWSRWSQESSVE 220
RESULT 15
I56563
interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia a
A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C:Genetics:

Search completed: September 1, 2001, 19:07:55
Job time: 122 sec .

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:25 ; Search time 24.79 Seconds
(without alignments)
473.967 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901

Sequence: 1 MAFVCLAGCLYFLISTTF.....EWSDKQWEGEDLSKTKLLR 343

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | DB ID | Description |
|------------|-------|---------|-------|--------|------------|---------------------|
| 1 | 1901 | 100.0 | 380 | 1 | I132_HUMAN | Q14627 homo sapien |
| 2 | 293.5 | 15.4 | 420 | 1 | IL5R_HUMAN | Q01344 homo sapien |
| 3 | 289.5 | 15.2 | 424 | 1 | I131_MOUSE | O09030 mus musculus |
| 4 | 285 | 15.0 | 427 | 1 | I131_HUMAN | P78552 homo sapien |
| 5 | 254 | 13.4 | 831 | 1 | PRLR_CHICK | O04594 gallus galli |
| 6 | 229 | 12.0 | 415 | 1 | IL5R_MOUSE | P21183 mus musculus |
| 7 | 228 | 12.0 | 831 | 1 | PRLR_MELGA | Q91094 meleagris g |
| 8 | 210.5 | 11.1 | 830 | 1 | PRLR_COLLI | Q90374 columba liv |
| 9 | 208 | 10.9 | 369 | 1 | CVRG_HUMAN | P31785 homo sapien |
| 10 | 206 | 10.8 | 373 | 1 | CVRG_CANFA | P40321 canis famil |
| 11 | 198.5 | 10.4 | 369 | 1 | CVRG_MOUSE | P34902 mus musculus |
| 12 | 187.5 | 9.9 | 379 | 1 | CVRG_BOVIN | Q95118 bos taurus |
| 13 | 179 | 9.4 | 878 | 1 | IL3B_MOUSE | P26954 mus musculus |
| 14 | 165 | 8.7 | 581 | 1 | PRLR_BOVIN | Q28172 bos taurus |
| 15 | 165 | 8.7 | 610 | 1 | PRLR_RAT | P05710 rattus norv |
| 16 | 160 | 8.4 | 897 | 1 | CVRB_HUMAN | P32927 homo sapien |
| 17 | 159 | 8.4 | 608 | 1 | PRLR_MOUSE | Q08501 mus musculus |
| 18 | 155.5 | 8.2 | 896 | 1 | CVRB_MOUSE | P26955 mus musculus |
| 19 | 151 | 7.9 | 622 | 1 | PRLR_HUMAN | P36471 homo sapien |
| 20 | 150.5 | 7.9 | 917 | 1 | IL6B_MOUSE | Q00560 mus musculus |
| 21 | 150 | 7.9 | 581 | 1 | PRLR_CEREL | Q28235 cervus elap |
| 22 | 147 | 7.7 | 616 | 1 | PRLR_RABIT | P14787 oryctolagus |
| 23 | 145.5 | 7.7 | 862 | 1 | I12S_HUMAN | Q99665 homo sapien |
| 24 | 133.5 | 7.0 | 400 | 1 | GMCR_HUMAN | P15509 homo sapien |
| 25 | 130.5 | 6.9 | 378 | 1 | IL3R_HUMAN | P26951 homo sapien |
| 26 | 128 | 6.7 | 630 | 1 | PRLR_ORENI | Q91513 oreochromis |
| 27 | 126.5 | 6.7 | 874 | 1 | I12S_MOUSE | P37378 mus musculus |
| 28 | 126.5 | 6.7 | 918 | 1 | IL6B_HUMAN | P40189 homo sapien |
| 29 | 123.5 | 6.5 | 1097 | 1 | LIFR_HUMAN | P42702 homo sapien |
| 30 | 113.5 | 6.0 | 1165 | 1 | LEPR_HUMAN | P48357 homo sapien |
| 31 | 112.5 | 5.9 | 1630 | 1 | PTPI_DROME | P35992 drosophila |
| 32 | 109.5 | 5.8 | 918 | 1 | IL6B_RAT | P40190 rattus norv |
| 33 | 107 | 5.6 | 634 | 1 | GHR_BOVIN | P79108 bos taurus |

RESULT 1
I132_HUMAN

| ID | I132_HUMAN | STANDARD; | PRT; | 380 AA. |
|----|--|-----------|------|---------|
| AC | Q14627; 000667; | | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) | | | |
| DE | INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 BINDING PROTEIN). | | | |
| GN | IL13RA2 OR IL13R. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Renal cell carcinoma; | | | |
| RX | MEDLINE=96279273; PubMed=8663118; | | | |
| RA | Caput D., Laurent P., Kaghad M., Lellias J.M., Lefort S., Vita N., Ferrara P.; | | | |
| RA | "Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain." | | | |
| RT | J. Biol. Chem. 271:16921-16926(1996). | | | |
| RL | [2] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RP | TISSUE=Testis; | | | |
| RC | Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.; | | | |
| RA | Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases. | | | |
| RL | [3] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RP | TISSUE=Brain; | | | |
| RC | MEDLINE=97321053; PubMed=9177784; | | | |
| RX | Guo J., Apion F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.; | | | |
| RA | "Chromosome mapping and expression of the human interleukin-13 receptor." | | | |
| RT | Genomics 42:141-145(1997). | | | |
| RL | -!- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13). BUT NOT TO IL-4. | | | |
| CC | -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. | | | |
| CC | -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN. | | | |
| CC | -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. | | | |
| CC | ----- | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL; X95302; CAA64617.1; -; | | | |
| DR | EMBL; U70981; AAB17170.1; -; | | | |
| DR | EMBL; Y08768; CAA70021.1; -; | | | |
| DR | MIM; 300130; -; | | | |

ALIGNMENTS

| | | | | | | |
|----|------|-----|------|---|------------|---------------------|
| 34 | 106 | 5.6 | 634 | 1 | GHR_SHEEP | Q28575 ovls aries |
| 35 | 105 | 5.5 | 837 | 1 | GCSR_MOUSE | P40223 mus musculus |
| 36 | 104 | 5.5 | 836 | 1 | GCSR_HUMAN | O99062 homo sapien |
| 37 | 99.5 | 5.2 | 638 | 1 | GHR_PIG | P19756 sus scrofa |
| 38 | 99.5 | 5.2 | 1162 | 1 | LEPR_RAT | Q62959 rattus norv |
| 39 | 98.5 | 5.2 | 1162 | 1 | LEPR_MOUSE | P48356 mus musculus |
| 40 | 97 | 5.1 | 1040 | 1 | AXOI_RAT | P22063 rattus norv |
| 41 | 96.5 | 5.1 | 396 | 1 | IL3A_MOUSE | P26952 mus musculus |
| 42 | 96.5 | 5.1 | 638 | 1 | GHR_HUMAN | P10912 homo sapien |
| 43 | 96.5 | 5.1 | 2499 | 1 | MPRI_BOVIN | P08169 bos taurus |
| 44 | 96 | 5.0 | 511 | 1 | VGLG_VSVO | P04884 vesicular s |
| 45 | 96 | 5.0 | 1705 | 1 | PTPO_MOUSE | P70289 mus musculus |

```
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3.1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B5562C887 CRC64;

Query Match 100.0%; Score 1901; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 7.1e-150;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTFELISTFGCTSSDTEIKVNPDPDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTFELISTFGCTSSDTEIKVNPDPDFEIVDPGVLGYLYLQWQPPLSLD 60

Qy 61 HFKECTVEYELKYNIGSETWKTITKLNHLKDGFDLNGKEAKIHTLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITKLNHLKDGFDLNGKEAKIHTLLPWOCTNGSEVQ 120

Qy 121 SSWAETTWISPOGIPETKVQDMDCVYVNWYLLCSWKPGVGLDNTNLYFYWVEGLDH 180
Db 121 SSWAETTWISPOGIPETKVQDMDCVYVNWYLLCSWKPGVGLDNTNLYFYWVEGLDH 180

Qy 181 ALQCVDYIKADQNGTCGRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLNIVRPLP 240
Db 181 ALQCVDYIKADQNGTCGRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLNIVRPLP 240

Qy 241 PVYLFTRESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLTATVENETYLTKTNE 300
Db 241 PVYLFTRESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLTATVENETYLTKTNE 300

Qy 301 TRQLCFVVRKVNICYSDGIGWSEWSDKQCEGDELKSKTLRL 343
Db 301 TRQLCFVVRKVNICYSDGIGWSEWSDKQCEGDELKSKTLRL 343

RESULT 2
ID IL5R_HUMAN
AC Q01344;
DC 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;

RT RT
RL RL
RN RN
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT for GM-CSF.";
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A26249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A28251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; 147851; -.
DR InterPro; IPR000950; -.
DR InterPro; IPR002465; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420
FT DOMAIN 21 342
FT TRANSMEM 343 362
FT DOMAIN 363 420
FT CARBOHYD 35 35
FT CARBOHYD 131 131
FT CARBOHYD 216 216
FT CARBOHYD 244 244
FT VARSPPLIC 333 335
FT VARSPPLIC 336 420
FT VARSPPLIC 333 333
FT VARSPPLIC 334 420
SQ SEQUENCE 420 AA; 47700 MW; 420681FEC6B51700 CRC84;

INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NDE -> FSR (IN SOLUBLE ISOFORM S1).
MISSING (IN SOLUBLE ISOFORM S1).
N -> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).

Query Match 15.4%; Score 293.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 4.8e-17;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;

Qy 27 DTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLDHFKECTVEYELKYNIGSETWKTIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRT 82

Qy 87 KNLHYKDGFDLNGKEAKIHTLLPWOCTNGSEWSSNAETTYWISPOGIPETKVQDMDCV 146
Db 83 ES---KCVTILHKGFSASVRTILO---NDHSLASSWASAEHL-APPSPGTSIVNLTCT 135
```

| FT | DISULFID | 132 | 142 | BY SIMILARITY. |
|-----|----------|---------|-----------|-------------------------------------|
| FT | DISULFID | 171 | 183 | BY SIMILARITY. |
| FT | CARBOHYD | 35 | 35 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 59 | 59 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 103 | 103 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 136 | 136 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 262 | 262 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 338 | 338 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| SEQ | SEQUENCE | 424 AA; | 48402 MW; | EB8330ADC82C9F9 CRC64; |

| Query Match | 15.2%; | Score 289.5; | DB 1; | Length 424; |
|-----------------------|------------------|------------------|------------|-------------|
| Best local Similarity | 25.8%; | Pred. No. 1e-16; | | |
| Matches 93; | Conservative 63; | Mismatches 131; | Indels 73; | Gaps |

| Qy | 8 | IGCLYTLFLIST-TFGCVSSSDTEKVNPPQDDEFIVDPGVLGYLVLOWQPLSLDHFKECT | 66 |
|--|--|---|-----|
| Db <td>7</td> <td>LGELLVLLWTATVGVA---TEVQPPVTNLSVSVENLCTIITWSPPEGAS--PNCT</td> <td>61</td> | 7 | LGELLVLLWTATVGVA---TEVQPPVTNLSVSVENLCTIITWSPPEGAS--PNCT | 61 |
| Qy <td>67<td>VEY-----ELKYRNIGSETWKTITIKNLNHYKDFDLNKGIEAKIHTLLPWQCT--NGSEVQ</td><td>120</td></td> | 67 <td>VEY-----ELKYRNIGSETWKTITIKNLNHYKDFDLNKGIEAKIHTLLPWQCT--NGSEVQ</td> <td>120</td> | VEY-----ELKYRNIGSETWKTITIKNLNHYKDFDLNKGIEAKIHTLLPWQCT--NGSEVQ | 120 |
| Db <td>62<td>LRVFSHFDDQDQKKAIPET-----HRKEELPLDEKICLQVGS----QCSANESEKP</td><td>108</td></td> | 62 <td>LRVFSHFDDQDQKKAIPET-----HRKEELPLDEKICLQVGS----QCSANESEKP</td> <td>108</td> | LRVFSHFDDQDQKKAIPET-----HRKEELPLDEKICLQVGS----QCSANESEKP | 108 |
| Qy <td>121<td>SSWAEITYWIS--PGIPIETKVQDMCVYVYVQVLLCSWKEGIGVLDLTNTNLYFYWEGLD</td><td>179</td></td> | 121 <td>SSWAEITYWIS--PGIPIETKVQDMCVYVYVQVLLCSWKEGIGVLDLTNTNLYFYWEGLD</td> <td>179</td> | SSWAEITYWIS--PGIPIETKVQDMCVYVYVQVLLCSWKEGIGVLDLTNTNLYFYWEGLD | 179 |
| Db <td>109<td>SPLVKKC--ISPPGDPESAVTELKCIWHNLSYMKCSWLPGRNTSPDTHYTLTYWYSLE</td><td>166</td></td> | 109 <td>SPLVKKC--ISPPGDPESAVTELKCIWHNLSYMKCSWLPGRNTSPDTHYTLTYWYSLE</td> <td>166</td> | SPLVKKC--ISPPGDPESAVTELKCIWHNLSYMKCSWLPGRNTSPDTHYTLTYWYSLE | 166 |
| Qy <td>180<td>HALQCDVIKADGONICGRFPYLEAS--DYKDFYICVNGSSSENKPIRSSYFTFQLONIY</td><td>236</td></td> | 180 <td>HALQCDVIKADGONICGRFPYLEAS--DYKDFYICVNGSSSENKPIRSSYFTFQLONIY</td> <td>236</td> | HALQCDVIKADGONICGRFPYLEAS--DYKDFYICVNGSSSENKPIRSSYFTFQLONIY | 236 |
| Db <td>167<td>KSROC--ENIVREGHIIACSPKLTKVESFQHNVQIMVKDNACK--IRPCKIVSLTSYV</td><td>223</td></td> | 167 <td>KSROC--ENIVREGHIIACSPKLTKVESFQHNVQIMVKDNACK--IRPCKIVSLTSYV</td> <td>223</td> | KSROC--ENIVREGHIIACSPKLTKVESFQHNVQIMVKDNACK--IRPCKIVSLTSYV | 223 |
| Qy <td>237<td>KPLPVVLTFTRESSCBIKLWSIPLGPPIPARCFDYIEIR-----</td><td>277</td></td> | 237 <td>KPLPVVLTFTRESSCBIKLWSIPLGPPIPARCFDYIEIR-----</td> <td>277</td> | KPLPVVLTFTRESSCBIKLWSIPLGPPIPARCFDYIEIR----- | 277 |
| Db <td>224<td>KPDPP-HIKHLLKNGALLVQWKNPON-FRSRCITYEVEVNTQTDHNLILEVEDKQCN</td><td>281</td></td> | 224 <td>KPDPP-HIKHLLKNGALLVQWKNPON-FRSRCITYEVEVNTQTDHNLILEVEDKQCN</td> <td>281</td> | KPDPP-HIKHLLKNGALLVQWKNPON-FRSRCITYEVEVNTQTDHNLILEVEDKQCN | 281 |
| Qy <td>278<td>-EDDTTL-----VTATVVENYETLTNTTNETQLCFVRSKNVNYCSDPGIINSEWSDKQ</td><td>329</td></td> | 278 <td>-EDDTTL-----VTATVVENYETLTNTTNETQLCFVRSKNVNYCSDPGIINSEWSDKQ</td> <td>329</td> | -EDDTTL-----VTATVVENYETLTNTTNETQLCFVRSKNVNYCSDPGIINSEWSDKQ | 329 |
| Db <td>282<td>SESDRNMEGTSFQOLPGVLADAVYTVRVKTNKLCF-----DDNKLWSDWSEAQ</td><td>331</td></td> | 282 <td>SESDRNMEGTSFQOLPGVLADAVYTVRVKTNKLCF-----DDNKLWSDWSEAQ</td> <td>331</td> | SESDRNMEGTSFQOLPGVLADAVYTVRVKTNKLCF-----DDNKLWSDWSEAQ | 331 |

| RESULT | 4 |
|-------------|---|
| IL131_HUMAN | |
| AC | IL131_HUMAN STANDARD; PRT; 427 AA. |
| ID | P78552; O96656; O95646; |
| DT | 01-NOV-1997 (Rel. 35, Created) |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) |
| DE | INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1). |
| GN | IL13RA1 OR IL13RA OR IL13R. |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| OX | NCBI_TaxID=9606; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=Carcinoma; |
| RX | MEDLINE=97165986; PubMed=9013879; |
| RA | Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N., |
| RA | Ferrara P.; |
| RT | "Cloning of the human IL-13R alpha chain and reconstitution with the |
| RL | IL4R alpha of a functional IL-4/IL-13 receptor complex."; |
| FL | FEBS Lett. 401:163-166(1997). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=B-cell; |
| RA | Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M., |
| RA | Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T., |
| RA | Eugster H.P., Bonnefoy J.Y.; |
| RL | Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases. |
| RN | [3] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=T-cell; |


```
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 830 AA; 94507 MW; 38074E83CDF69EFF CRC64;

Query Match 11.1%; Score 210.5; DB 1; Length 830;
Best Local Similarity 24.7%; Pred. No. 7.9e-10;
Matches 86; Conservative 47; Mismatches 156; Indels 59; Gaps 14;

Qy 18 TFGCTSSDTEIKVNPQDPEIVDPGVLG-----DPQYVDVTIVQDPVNLSTKTSASTYLLAKW 150
Db 97 TTYNITVNMAMEIGSNSS-----DPQYVDVTIVQDPVNLSTKTSASTYLLAKW 150

Qy 54 QPPLSLDHFKECTV-EYELKRYNTGSETWKTIIYNLHYKDFGLNKIGIEAKIHTLLPWQ 112
Db 151 SPPLADVTSHVYRELRLKPEKEWETV---SVGVOYQYKVNRLQAGVYVQVQR 206

Qy 113 CTNGSEVSSAETTYTISPOG-IPETRVQDMDCVYVNNQYLLCSWKPGIGVLLDTNYNL 171
Db 207 CVLDIGENSESSERHIHPNGESFPEKPTTIKCRSPKEFTTCWKPDSGGHPTNTYL 266

Qy 172 FYWTEGLDHALQVDYIKADGONTGCRFPYLEADYKDFYICVNGSSSENKPIRSYFTFFQ 231
Db 267 LYSKEGEERVVECPDY-KTAGPN-SCYPDKKHTSFWTIYNITVRATNEIGSNVSDPLYVD 324

Qy 232 LQNIKVPPLPVYLTFTRESSCEIK-----LKWS-IPLGPIPA--RCFDYEIREDDTTLV 284
Db 325 VTYIVQTPPPVNVNLTLEKTKTVNRKPYLVLTWSPPLADVRSGWLTFLDYELRLKPEEA--- 381

Qy 285 TATVENETYTLTKTNRQLCFVW-----RSKNVNYCSDD--GIWSEWS 326
Db 382 -----EWEETIFVGOOTHYKMFSLNPGKKYIVQIHCKPDHGHGNSWS 424

RESULT 9
CYRG_HUMAN
ID CYRG_HUMAN STANDARD; PRT; 369 AA.
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-
DE 2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN).
GN IL2RG
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=1631559;
RA Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor.";
RL Science 257:379-382(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93293887; PubMed=8514792;
RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;
RT "Characterization of the human interleukin-2 receptor gamma chain
RT gene.";
RL J. Biol. Chem. 268:13601-13608(1993).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
```

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RX MEDLINE=94004847; PubMed=8401490;
RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
RA Willard H., Henthorn P.S.;
RT "The interleukin-2 receptor gamma chain maps to Xql3.1 and is mutated
RL in X-linked severe combined immunodeficiency, SCIDX1.";
Hum. Mol. Genet. 2:1099-1104(1993).
RN [4]
RP IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090315; PubMed=8266076;
RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
RA Arai K.-I., Sugamura K.;
RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
RL receptors for IL-2 and IL-4.";
Science 262:1874-1877(1993).
RN [5]
RP IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090317; PubMed=8266078;
RA Russell S.M., Kkegan A.D., Harada N., Nakamura Y., Noguchi M.,
RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-4 receptor.";
Science 262:1880-1883(1993).
RN [6]
RP IDENTIFICATION AS A IL-7R SUBUNIT.
RX MEDLINE=94090316; PubMed=8266077;
RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-7 receptor.";
Science 262:1877-1880(1993).
RN [7]
RP 3D-STRUCTURE MODELING OF 57-248.
RX MEDLINE=95111955; PubMed=7529123;
RA Bamorough P., Hedgecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
RL modelling.";
Structure 2:839-851(1994).
RN [8]
RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
RX MEDLINE=94130970; PubMed=8299698;
RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
RA de Saint Basile G.;
RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
RL severe combined immunodeficiency disease result in the loss of
RL high-affinity IL-2 receptor binding.";
Eur. J. Immunol. 24:475-479(1994).
RN [9]
RP VARIANT XSCID LYS-68.
RX MEDLINE=94375038; PubMed=8088810;
RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Detection of three nonsense mutations and one missense mutation in
RL the interleukin-2 receptor gamma chain gene in SCIDX1 that
RL differently affect the mRNA processing.";
Genomics 21:291-293(1994).
RN [10]
RP VARIANT XSCID HIS-162.
RX MEDLINE=94300093; PubMed=8027558;
RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
RT "Impairment of ligand binding and growth signaling of mutant IL-2
RL receptor gamma-chains in patients with X-linked severe combined
RL immunodeficiency.";
J. Immunol. 153:1310-1317(1994).
RN [11]
RP VARIANT XSCID ASN-39.
RX MEDLINE=95023932; PubMed=7937790;
RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Defective human interleukin 2 receptor gamma chain in an atypical X
RL chromosome-linked severe combined immunodeficiency with peripheral T
RL cells.";
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disease.";
RL Genomics 23:69-74(1994).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U04361; AAC48403.1; -
DR HSSP; P31785; 1ILN.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_SF_1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 373 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 261 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 262 283 POTENTIAL.
FT DOMAIN 284 373 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 249 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1FB089D8B CRC64;
Query Match 10.8%; Score 206; DB 1; Length 373;
Best Local Similarity 27.3%; Pred. No. 7e-10;
Matches 67; Conservative 42; Mismatches 100; Indels 36; Gaps 11;
QY 115 NGSE-----VQSSWAETTYWISPGIPETKVQDMDCVYNNWQYLLCSW-----KPGI 161
Db 31 NGNEDITPDDFTATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSEPRP-- 82
QY 162 GVLLDTNLYFWYBGL--DHALQCVDYIKADGQGNIGCRFPYLEASDYKDFVCVNGSSE 219
Db 83 -----TNLTLYHWYKNSNDKRVQEGCHLFSEVYTAGCWLQKEEHLHYETFWQLRDRPE 137
QY 220 NKPIRSSFTTQQLNIVPLPPVYITFTRESCEIKLKWISPLGIPARCFDYEIEIRD 279
Db 138 --PRQSQTKLQKLQNLVWPAPENLTNLNLSQESLWS---NRHLDHCLHEHVQVRS 192
QY 280 -DTTLVATVEN-EYITLKTNETPQLCFVVRKSNVNYCSDGIWSESDKQCEGDEL 337
Db 193 WDRSMTEQSDVHRNFSFLPSVDGQKFTFYVRKSRYNPLCSQAQRWSESHPIHW-GSNTS 251
QY 338 KKTLL 342
Db 252 KENPL 256
RESULT 11
CYRG_MOUSE

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ID AC CYRG_MOUSE STANDARD; PRT; 369 AA.
DT DT P34902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors.";
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/CA;
RX MEDLINE=93391374; PubMed=8378320;
RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RT IL-2R gamma chain expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma.";
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT chromosomal localization and expression in the adult thymus.";
RL Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S;
RX MEDLINE=96341745; PubMed=8750189;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44.";
RL J. Neurooncol. 26:231-239(1995).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D13821; BAA02974.1; -
DR EMBL; U21795; AAA64279.1; -
DR EMBL; D13565; BAA02760.1; -
DR EMBL; L20048; AAA39286.1; -

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DR EMBL; S75852; AAB32904.1; -.
DR EMBL; S75844; AAB32904.1; JOINED.
DR EMBL; S75845; AAB32904.1; JOINED.
DR EMBL; S75847; AAB32904.1; JOINED.
DR EMBL; S75848; AAB32904.1; JOINED.
DR EMBL; S75849; AAB32904.1; JOINED.
DR EMBL; S75850; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR EMBL; X75337; CAA53085.1; -.
DR PIR; JN0592; JN0592.
DR PIR; JN0775; JN0775.
DR HSSP; P31785; IL1N.
DR MGD; MGI:96551; IL2rg.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 22
FT CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 264 284
FT DOMAIN 285 369
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 369 AA; 42241 MW; CB2DSAB459077AC7 CRC64;

Query Match 10.4%; Score 198.5; DB 1; Length 369;
Best Local Similarity 26.5%; Pred. No. 2.9e-09;
Matches 54; Conservative 38; Mismatches 95; Indels 17; Gaps 7;

QY 136 PETKVQDMDCVYVNWYLLCSW----KPGIGVLLDTNLYNLFYVY---EGLDHALQCV 189
Db 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPQA-----TNLTLYRYKVSNDNTFFQECSHYLF 107

QY 190 ADGQNGICRFPYLEASDYICVNGSENKPIRSYFTFQLQNIYKPLPPVYLTRE 249
Db 108 SKEITSGCQIQEKEDQLYQTFVQL--QDPQKQPRRAVQKLNQLNLYIPRAPENLTLSNL 165

QY 250 SSECILKWSIPLGPIPARCFDYIEIREDDTLVLTATVENE--TYTLKTTNTRQLCFV 307
Db 166 SESQLELRWK--SRHIKERCLQLYVQRNDRSGTWELIVNHEPRFSLPSVDLKRVTFR 223

QY 308 VRSKVNIYCSDDGIWSEWSKQCV 331
Db 224 VRSRYNPICGSSQWQKWSQPVHW 247

RESULT 12
CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR COMMON GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

```

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RP SEQUENCE FROM N.A.
RX MEDLINE=96268473; PubMed=8672241;
RA YOO J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
gamma gene.";
RL DNA Cell Biol. 15:453-459(1996).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC -----
DR EMBL; U33748; AAB07812.1; -.
DR HSSP; P31785; IL1N.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 22
FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290
FT DOMAIN 291 379
FT DISULFID 158 256
FT DISULFID 109 122
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.9%; Score 187.5; DB 1; Length 379;
Best Local Similarity 26.1%; Pred. No. 2.4e-08;
Matches 57; Conservative 41; Mismatches 93; Indels 27; Gaps 9;

QY 135 IPETKVQDMDCVYVNWYLLCSW----KPGIGVLLDTNLYNLFYVY---EGLDHALQCV 185
Db 61 LPLPKVQ---CFVFNVEYMNCTWNSSEPQA-----NNLTLYRYNFGDDKLECG 110

QY 186 DYKADQNGICRFPYLEASDYICVNGSENKPIRSYFTFQLQNIYKPLPPVYLT 245
Db 111 HYLFSGITSGCWFQKKEIRLYETFFVQLQDPREHR--KQPKQMLQLDLVWPAPENLT 168

QY 246 FTRESCEILKWSIPLGPIPARCFDYIEIREDDTLVLTATVENE--TYTLKTTNTRQ 303
Db 169 LRNLSEFQLELSWS---NRYLDHCHLEHLVQYRSDRDSRWTEQSYDHRHSFSLPSVDAQKL 225

QY 304 LCFVVRSKVNIYCSDDGIWSEWSKQCV 341
Db 226 YTFVRSRYNPICGSAQHWSDWSYPIHW--GSNTSKENI 262

RESULT 13
IL3B_MOUSE
ID IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)

```

[illegible]

QY 191 DQONIGCREPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLONIWKPLPPVYL 245
Db 76 SGN-SCPFQYTSWKYIITVNTNMGSSSDPL-----YVDVTYIVEPEPRNL 129
QY 246 F-----TRESSCEIKLWSIP-LGPIPARCFDYEIREDDTTLVTATVENETYTLKTTNE 300
Db 130 LEVKOLKDKTYLWKWSPTTIDVKGTGFTMEYER-----LKPEAEWEIHFTH 182
QY 301 TRQL-----CFVRSKNYICSDDGWSEWSDKQCWE 332
Db 183 QTQFKVEDLYPCQKYLVTOTCK---PDHGYWRSQESSVE 220

Search completed: September 1, 2001, 19:16:26
Job time: 508 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:15:53 ; Search time 68.62 seconds
(without alignments)
661.332 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901

Sequence: 1 MAFVCLAIGCLYFLISTTF.....EWSDKQCWGEDLSKTKTLR 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1184 | 62.3 | 383 | 11 | O88786 |
| 2 | 294.5 | 15.5 | 420 | 4 | Q14633 mus musculus |
| 3 | 293.5 | 15.4 | 396 | 4 | Q14631 homo sapien |
| 4 | 292 | 15.4 | 333 | 4 | Q15469 homo sapien |
| 5 | 284.5 | 15.0 | 415 | 11 | Q920K4 |
| 6 | 260 | 13.7 | 349 | 6 | Q97597 bos taurus |
| 7 | 241.5 | 12.7 | 279 | 4 | Q9UDY5 |
| 8 | 190.5 | 10.0 | 363 | 13 | Q9DEQ1 |
| 9 | 173.5 | 9.1 | 881 | 13 | Q57519 |
| 10 | 167 | 8.8 | 611 | 13 | Q9PTI0 |
| 11 | 167 | 8.8 | 611 | 13 | Q9IBF6 |
| 12 | 167 | 8.8 | 622 | 6 | Q9N0J7 |
| 13 | 165 | 8.7 | 296 | 6 | Q18880 |
| 14 | 165 | 8.7 | 896 | 11 | Q64146 |
| 15 | 159.5 | 8.4 | 890 | 11 | Q9Z1A0 |
| 16 | 159 | 8.4 | 227 | 6 | Q9GLW3 |
| 17 | 157 | 8.3 | 581 | 6 | O46561 |
| 18 | 156 | 8.2 | 625 | 6 | Q9XS92 |
| 19 | 154.5 | 8.1 | 611 | 13 | Q9PTH9 |

| | | | | | |
|----|-------|-----|-------|----|--------|
| 20 | 151 | 7.9 | 206 | 4 | Q16354 |
| 21 | 151 | 7.9 | 349 | 4 | Q9UHJ5 |
| 22 | 147.5 | 7.8 | 538 | 13 | Q9DFU0 |
| 23 | 146.5 | 7.7 | 422 | 4 | Q9UHH5 |
| 24 | 145.5 | 7.7 | 217 | 6 | O46386 |
| 25 | 145.5 | 7.7 | 422 | 4 | O75462 |
| 26 | 143.5 | 7.5 | 425 | 11 | Q9JM58 |
| 27 | 143.5 | 7.5 | 918 | 13 | Q9W6U9 |
| 28 | 132 | 6.9 | 346 | 13 | Q93404 |
| 29 | 130.5 | 6.9 | 198 | 6 | O18985 |
| 30 | 130.5 | 6.9 | 390 | 4 | Q9UEH7 |
| 31 | 126.5 | 6.7 | 329 | 4 | Q9UQ41 |
| 32 | 117.5 | 6.2 | 896 | 4 | Q13594 |
| 33 | 117.5 | 6.2 | 906 | 4 | Q13593 |
| 34 | 117.5 | 6.2 | 958 | 4 | Q13592 |
| 35 | 116.5 | 6.1 | 1282 | 5 | Q9WFE0 |
| 36 | 114 | 6.0 | 371 | 4 | Q9HC73 |
| 37 | 114 | 6.0 | 894 | 6 | Q9MYL1 |
| 38 | 114 | 6.0 | 925 | 6 | Q9MYK9 |
| 39 | 114 | 6.0 | 1163 | 6 | Q9MYL2 |
| 40 | 114 | 6.0 | 1194 | 6 | Q9MYL0 |
| 41 | 113.5 | 6.0 | 896 | 4 | Q92919 |
| 42 | 113.5 | 6.0 | 958 | 4 | Q92920 |
| 43 | 113.5 | 6.0 | 1165 | 4 | Q92921 |
| 44 | 109.5 | 5.8 | 26926 | 4 | Q10466 |
| 45 | 109 | 5.7 | 2221 | 5 | Q9U1M1 |

ALIGNMENTS

RESULT 1

O88786 PRELIMINARY; PRT; 383 AA.

AC O88786;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE IL-13 RECEPTOR ALPHA 2.

GN IL13RA2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/HEJ; TISSUE=THYMUS;

RX MEDLINE=98391042; PubMed=9725226;

RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,

RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,

RA Collins M.;

RT "The murine IL-13 receptor alpha 2: molecular cloning,

RT characterization, and comparison with murine IL-13 receptor alpha 1.";

RL J. Immunol. 161:2317-2324(1998).

DR EMBL; U65747; AAC33240.1; -

DR MGD; MGI:1277954; I113ra2.

DR InterPro; IPR002596; -

DR InterPro; IPR003532; -

DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.

SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 62.3%; Score 1184; DB 11; Length 383;

Best Local Similarity 64.0%; Pred. No. 1.1e-99;

Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYFLISTTFGCTSSSDTEIKVNPQDFIVDPGYLYLQWPPPLSD 60

Db 1 MAFV-HRCLCFLICITIGYS----LEIKVNPQDFEILDGLGYLYLQWPPVWIE 54

QY 61 HFPECTVEYELKRNIGSETWTKTITIKNLHYKDGFDLKNKGIEAKIHTLPLWQCTNGSEVQ 120

Db 55 KFKGCTLEYELAYRNVDSDSWKTIITRNLIYKDGFDLKNKGIEGKIRTHLSEHCTNGSEVQ 114

[illegible]

DR InterPro: IPR002996; -
DR InterPro: IPR003532; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA.
SQ SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match 15.0%; Score 284.5; DB 11; Length 415;
Best Local Similarity 27.4%; Pred. No. 8.1e-18;
Matches 93; Conservative 55; Mismatches 149; Indels 43; Gaps

| | | |
|----|-----|--|
| QY | 6 | L A I G C L Y T F L I S T F T G C T S S D T E I K V N P Q D F E I Y D P G Y G L Y L Q W O P P L S L D H F K E C 65 |
| | | : : : : : : : : : : : : : : |
| DB | 7 | I L L G A I E T L Q D T L -----P D K K F L L P P I N F T I K V T G -L A Q V L C W E P N P Q G -K N V 56 |
| | | : : : : : : : : : : : : : : |
| QY | 66 | T V E Y E L K Y R I G S E T W K T I T K N L H Y K D G F L N K G E A K I H T I L L P Q C I N G S E V Q S W A E 125 |
| | | : : : : : : : : : : : : : : |
| DB | 59 | N L A Y H V K I N P Q E E D Y E -----T R N T Q S K E T F L H G G V S A S V R T L -W H --G H S L A S S W S 112 |
| | | : : : : : : : : : : : : : : |
| QY | 126 | T T W I S P Q I P E T K V Q D M D C V -----Y Y N W Q -----Y L L C S W K P G I G V L L D T N Y N L F Y - 173 |
| | | : : : : : : : : : : : : : : |
| DB | 113 | A E H -K A P P G S G T S I V N L T C T T T A S N Y T N L K S Y E V S L H C T W L A G K D A P E D T Q Y F L Y R 171 |
| | | : : : : : : : : : : : : : : |
| QY | 174 | --W Y E G L D H A L O C V D Y I K A D -Q O N T G C R P P --Y L E A S D Y K D F Y I C V N G S S E N K P I R S S Y 227 |
| | | : : : : : : : : : : : : : : |
| DB | 172 | Y G P W T E -----E C Q E Y S K D T L S R N T A C W P R T F I H S K A R D R L A V H V N G S S N H A T I K P F D 225 |
| | | : : : : : : : : : : : : : : |
| QY | 228 | F T Q L Q N I V K P L P P V I L T F T R E S S C E K L K W S I P L G P I P A R C F D Y E I E I -R E D D T T L Y T A 286 |
| | | : : : : : : : : : : : : : : |
| DB | 226 | O L F D T Q A I D Q P N P M D V T A E T E G S -R L S I O M Q R P V S A F P I H C F E Y E V K I C N T K D Y O V E K 284 |
| | | : : : : : : : : : : : : : : |
| QY | 287 | T V E N E T Y L K T T N E T R O L C F W R S K V N I Y S D D G I N S E W S 326 |
| | | : : : : : : : : : : : : : : |
| DB | 285 | T T T N A -F V S T T D G V S Y S I Q V R A A V S P H C R A M G L S K W S 322 |
| | | : : : : : : : : : : : : : : |

RESULT 6
ID Q97597 PRELIMINARY; PRT; 349 AA.
AC OS7597;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.L., Hirano A., Brown W.C., Estes D.M.;
RT "Biological activities of interleukin-13 on bovine lymphocytes:
RT implications for signaling through IL-13Ra1.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RL ENBL; AF074402; AAC98147.1; -
DR InterPro: IPR002996; -
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT SEQUENCE 349 AA; 39644 MW; D61AAC918B19A0A6 CRC64;
SQ SEQUENCE 349 AA; 39644 MW; D61AAC918B19A0A6 CRC64;

Query Match 13.7%; Score 260; DB 6; Length 349;
Best Local Similarity 25.7%; Pred. No. 1.1e-15;
Matches 78; Conservative 53; Mismatches 120; Indels 52; Gaps 14;

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QY 53 WOPPLSLDHFKECTVEYELKYNIGSETWKTITIKNLHYKDFDLNKGIEAKIHTLLPWQ 112
Db 18 WNPPEGAS--PNCSLKY---FSHFGKQDKKIAPT-HRSKEVPLNERICLQVGS---Q 67
QY 113 C-TNGSEVQSSWAETTYWISQGPETKVDQMDCVYVWQYLLCSWKPGIGVLLDTNVL 171
Db 68 CSTNESEKPSILVEKCF-SPPEGDPESAVALQCIWHNLRMYKCTWLPGRNASPDPNYL 126
QY 172 FYWYEGDLHALQCVDYIKADGONICRPPYLEASD--YKDFYICVNGSSSENKPIRSSYFT 229
Db 127 YWHSNLSKGIQCFNFR-EGQHACSNLTKVKRDSFEQHSQVQVWVRDNGAGKISPSFNI 185
QY 230 FOLQNVKPLPPVYLTTRESSECEIKLWSIPLGPIPARCFDYEIFEIREDDTTTLVATVE 289
Db 186 VBLTSHVRP-DPSHIKLSFGQDLVQWTPQN-FQSQCLCYEVEVINSHA----- 235
QY 290 NETYTLTKTINETR-----QLCFVY-----RSKNVIYC-SDDGIWS 323
Db 236 -ETHDIFYVEAKQNTFEGNLEGTCFVMPVGLPDLTNTVIRVKTNKLCEYEDDKLWS 294
QY 324 EWS 326
Db 295 NWS 297
RESULT 7
Q9UDY5 PRELIMINARY; PRT; 279 AA.
AC Q9UDY5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81380; ADO0511.2; -.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR002996; -.
DR InterPro; IPR003532; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;
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Query Match 12.7%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 4e-14;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;
QY 11 LYTFLLSTFTGCTSSDTEIKVNPQDPEIYDPGYLYLQWOPPLSLDHFKECTVEY- 69
Db 10 LWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVITWNPPEGAS--SNCSLWYF 67
QY 70 ---ELKYNIGSETWKTITIKNLHYKDFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124
Db 68 SHFGQDKKKTAPETRRSI-----EVLNERICLQVGS---QCSTNESEKPSILV 114
QY 125 ETTYWIS-POGIPETKVDQMDCVYVWQYLLCSWKPGIGVLLDTNLYNLFYWYEGDLHALQ 183
Db 115 EKC--ISPEGDPESAVALQCIWHNLSYKCSNLPGRNTSPDNTYLYWHSLEKIHQ 172
QY 184 CVDYIKADGQNGICRPPYLEASD--YKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLPP 241
Db 173 C-ENIFREGQYFGGFSDLTKVKDSFEQHSQIMVKDNAGKIKPSFNIVPLTSRVKPDPP 231
QY 242 --VYLTTRESSECEIKLWSIPLGPIPARCFDYEIFEIREDDT 281
Db 232 HIKNLSFHND---DLYQVQENPQNF1-SRCLFYEVVNNSTQ 269
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RESULT 8
Q9DEQ1 PRELIMINARY; PRT; 363 AA.
AC Q9DEQ1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T., Secombes C.J.;
RT *Cloning and expression of the first non-mammalian cytokine receptor
RT common gamma chain gene in rainbow trout (Oncorhynchus mykiss).;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 363 AA; 41861 MW; DF69B2EB3EEA06D3 CRC64;
```

```
Query Match 10.0%; Score 190.5; DB 13; Length 363;
Best Local Similarity 22.9%; Pred. No. 2.4e-09;
Matches 55; Conservative 48; Mismatches 118; Indels 19; Gaps 6;
QY 97 LNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVDQMDCVYVWQYLLCS 156
Db 1 IHKIVRVELVTLIPTVTHFDKMKVGSW--LFLLSLQGYEAPSTPNVNCILINDYVNCI 58
QY 157 WKPGIGVLLDTNLYNLFYWYEGDLHALQCVYIKADGQNGICRPPYLEASDYKDFYICVNG 216
Db 59 WSE--QSIPEVNTFFSSRFIKDNMECTTYLQESYAVGCRSLSYDKSRDRF----- 108
QY 217 SSENKPIRSSYFTFQ---LQNVKPLPPVYLTTRESSECEIKLWSIPLGPIPARCFDYE 273
Db 109 TLTKLVHQNMSYVQDHNLSKMWKLYPPVNLVSVMKNKDPNLNLYNNNSKNFTF---CIESE 165
QY 274 IEIREDDTTLVTATVENE-TYTLKTTNETROLCFVRSKVNICYSDDGISWSDKQWCE 332
Db 166 VRYRNSDKWKTSTPSKEQKAVAFPLKSSRYEQVRRVNDMCGESEFNSWSPQIOWD 225
RESULT 9
O57519 PRELIMINARY; PRT; 881 AA.
AC O57519
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GPL30P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC0531.1; -.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
```

DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 9.1%; Score 173.5; DB 13; Length 881;
Best Local Similarity 25.0%; Pred. No. 2.6e-07;
Matches 75; Conservative 37; Mismatches 115; Indels 73; Gaps 14;

QY 68 EYELKYNIGSTWKTITIKNLHYKDGFLNGKIEAKIHTLLPWQCTNGSEVQSSWAET 127

DB 74 QYEILNQTTSSVTFFENLTILN-----SPLTCNVASGHV-----ANVL 111

QY 128 YMT-SQGIPIETKQVDMDCVYNNQYLLCSWKPGLVLDNTNLFY-W-YEGLDHALQC 184

DB 112 YGIFFTGLPPDKPTNLTCIVNQDNLTCTWDPGRPTNLPTNTLSHRWFGANY---- 167

QY 185 VDIKADQNGICRPPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIYKPLPPYV- 243

DB 168 -----CRGANNSTHTSPGFQFYIDTTFQVEATNELGIQKSETLTIDPYNIVKPNPPQLS 222

QY 244 -LTFRTRESSCEIKLWSIPLGPI-----PARCFDYEIEIREDDTTLVTATVENET 292

DB 223 ELISSELEPNALKIEKNPITAFNLKYNIRPVKTQDWEM-VEEDI-----ASHRDS 276

QY 293 YTLK-----TTNETRQLCFVVRKSVNIYCSDDGIWSEWSD--KQCW-----EGEDLSKK 339

DB 277 FTQLDLLPNTVVEVSIRC-----IHKDGHGFWSDWSELKQVTPPEAPPSRGPDWKK 328

RESULT 10

ID Q9PTIO PRELIMINARY; PRT; 611 AA.

AC Q9PTIO;

DT 01-MAY-2000 (TREMREL. 13, Created)

DT 01-MAY-2000 (TREMREL. 13, Last sequence update)

DE PROLACTIN RECEPTOR A.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8335;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20087225; PubMed=10618394;

RA Huang H., Brown D.D.

RT "Prolactin is not a juvenile hormone in Xenopus laevis

metamorphosis.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).

DR EMBL; AF193800; AAF05776.1; -.

DR HSSP; P16471; 1BP3.

DR InterPro; IPR001777; -.

DR InterPro; IPR002996; -.

DR Pfam; PF00041; fn3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.

DR SMART; SM00060; FN3; 1.

KW Receptor.

SQ SEQUENCE 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match 8.8%; Score 167; DB 13; Length 611;

Best Local Similarity 27.6%; Pred. No. 6.4e-07;

Matches 64; Conservative 30; Mismatches 100; Indels 38; Gaps 10;

QY 127 TYWISQGIPIETKQVDMDCVYNNQYLLCSWKPGLVLDNTNLFYWYEGLDHALQCVD 186

DB 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGLVLDNTNLFYWYEGLDHALQCVD 80

QY 187 YIKADQNGICRPPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFQLONIYKPL 239

DB 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVNNATLGSNVSDEESVDITY-----IVQPY 131

QY 240 PPVYLTFRTRESS-CEIKLWSIPLGPIPARCFD-----YEIEIRDDTTLVTATVE 289

DB 132 PPTNVSLAVESGHHDLLK-----LPPAMVDVQSGWLTALAYEVRYKEEQWEAHLV 185

QY 290 NETYLKTTNETRQLCFVVRKSVNIYCS-DDGIWSEWSDKQWEGEDLSKKT 340

DB 186 GNQLKLFGLTPGGNVVQ----VRCKPDSGHWSEWSTESYIQIPGGGKKT 233

RESULT 11

ID Q9IBF6 PRELIMINARY; PRT; 611 AA.

AC Q9IBF6;

DT 01-OCT-2000 (TREMREL. 15, Created)

DT 01-OCT-2000 (TREMREL. 15, Last sequence update)

DT 01-MAR-2001 (TREMREL. 16, Last annotation update)

DE PROLACTIN RECEPTOR.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8335;

RN [1]

RP SEQUENCE FROM N.A.

RA Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;

RT "Cloning of a cDNA for Xenopus prolactin receptor and its

metamorphophic expression profile.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB030443; BAA90400.1; -.

DR InterPro; IPR001777; -.

DR InterPro; IPR003528; -.

DR Pfam; PF00041; fn3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.

DR SMART; SM00060; FN3; 1.

KW Receptor.

SQ SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

Query Match 8.8%; Score 167; DB 13; Length 611;

Best Local Similarity 27.6%; Pred. No. 6.4e-07;

Matches 64; Conservative 30; Mismatches 100; Indels 38; Gaps 10;

QY 127 TYWISQGIPIETKQVDMDCVYNNQYLLCSWKPGLVLDNTNLFYWYEGLDHALQCVD 186

DB 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGLVLDNTNLFYWYEGLDHALQCVD 80

QY 187 YIKADQNGICRPPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFQLONIYKPL 239

DB 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVNNATLGSNVSDEESVDITY-----IVQPY 131

QY 240 PPVYLTFRTRESS-CEIKLWSIPLGPIPARCFD-----YEIEIRDDTTLVTATVE 289

DB 132 PPTNVSLAVESGHHDLLK-----LPPAMVDVQSGWLTALAYEVRYKEEQWEAHLV 185

QY 290 NETYLKTTNETRQLCFVVRKSVNIYCS-DDGIWSEWSDKQWEGEDLSKKT 340

DB 186 GNQLKLFGLTPGGNVVQ----VRCKPDSGHWSEWSTESYIQIPGGGKKT 233

RESULT 12

ID Q9NOJ7 PRELIMINARY; PRT; 622 AA.

AC Q9NOJ7;

DT 01-OCT-2000 (TREMREL. 15, Created)

DT 01-OCT-2000 (TREMREL. 15, Last sequence update)

DT 01-MAR-2001 (TREMREL. 16, Last annotation update)

DE PROLACTIN RECEPTOR PRECURSOR.

OS Callithrix jacchus (Common marmoset).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.

OX NCBI_TaxID=9483;

RN [1]

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RP SEQUENCE FROM N.A.
RA Dairyple A., Edery M., Jabbour H.;
RT "Sequence and functional characterisation of the marmoset monkey
RT (Callithrix jacchus) prolactin receptor: comparative homology with the
RT human long form prolactin receptor."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ272217; CAB75847.1; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam; PF00041; fn3; 2
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW SIGNAL; Receptor.
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 622 PROLACTIN RECEPTOR.
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6D6DB6 CRC64;

Query Match 8.8%; Score 167; DB 6; Length 622;
Best Local Similarity 28.8%; Pred. No. 6.6e-07;
Matches 61; Conservative 26; Mismatches 91; Indels 34; Gaps 10;

QY 131 SPQGPETKQVDMDCVYNNQYLLCSWPKGIGVLLDTNLYFYWYEGDLHALQCVDYKKA 190
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 26 SPFGKPEI----FKCRSPNKETTCWRPGADGGLPTNYSLAYHKEGEKFIHECPDYV--T 80
QY 191 DGONTGCRPPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLPPVYLTFRES 250
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 81 GGNP-SCHGKQYTSWRYIITVATNEMGSLDEIYVDVYIVEDPPUNVY----- 134
QY 251 SCEIK-----LKWSIP-LGPIPARCFD--YEIEIREDDTLVLTATVENETYLTKT 297
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 135 -VEVQPEDKPKYLVKWSPPPLDLKTGWFTLLYVQLKPNAB-----EMETHFAQ 187
QY 298 TNETROLCFVRSK--VNIYCS-DGIGSEWS 326
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 188 QTDKVLSLHPGQKYLQVVRCKPDHGYWSSWS 219

RESULT 13
O18880 SEQUENCE FROM N.A.
ID O18880 PRELIMINARY; PRT; 296 AA.
AC O18880
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97375450; PubMed=9231767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RT tissues."
RL Endocrinology 138:3187-3194(1997).
DR EMBL; AF027403; AAB83999.1; -
DR HSP; P14787; IAN3.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 296 AA; 33854 MW; 9F1C15FB41DE0787 CRC64;

Query Match 8.7%; Score 165; DB 6; Length 296;
Best Local Similarity 31.3%; Pred. No. 4e-07;
Matches 77; Conservative 62; Mismatches 156; Indels 80; Gaps 18;

QY 5 CLATGCL--YT-FLISTTFTGCTSSSDTEIKVN-----PPQFEIVDVGILYL 49
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 94 CVPRRCVLPYTFQFSVKEDYISLQDRDLSTHLVPLAQHVQPPPKDISPSGS--DHF 151
QY 50 YLQWQPPPL---SLDHFKECTVEYELKYNIGSETWKTITIKNLHYKDFDLNKGTEAKIH 106
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 152 LLKWSVPLGDAQVSLLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWLTLEPK 203
QY 107 TLLP-----WQCTNGSEVQ---SSWAETTWISQGPETKQVDMDCVYNNQYLL 154
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

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Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;

QY 136 PETKQVDMDCVYNNQYLLCSWPKGIGVLLDTNLYFYWYEGDLHALQCVDYKKA 195
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 27 PPEKPLVKCRSPGKETTCWRPGADGGLPTNYSLAYHKEGETLIHECPDY-KTGGPN- 84
QY 196 GCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLPPVYLTFRES 255
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 85 SCYFSKHTSIWKMYITVAINQMGISSDPLYYVHVYVIVEPEPPANLTLELKHPEDRK 144
QY 256 ---LKWSIP-LGPIPARCFD--YEIEIREDDTLVLTATVENET-YLTKTN-ETROL 306
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 145 PYLWIKWSPPTMTDVKSGWFIQYIRLKPKEAT-----DWETHFTLKQTLKIFNLYP 198
QY 307 VVRKVNIVCS-DDGIWSEWS 326
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 199 GOKYLVQIRCPDHGYWSEWS 219

RESULT 14
O64146 SEQUENCE FROM N.A.
ID O64146 PRELIMINARY; PRT; 896 AA.
AC O64146
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3R<BETA>
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo."
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; S79263; AAB35068.1; -
DR EMBL; AJ000555; CAA04186.1; -
DR InterPro; IPR000282; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT NON_TER 1 1
FT NON_TER 896 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match 8.7%; Score 165; DB 11; Length 896;
Best Local Similarity 20.5%; Pred. No. 1.6e-06;
Matches 77; Conservative 62; Mismatches 156; Indels 80; Gaps 18;

QY 5 CLATGCL--YT-FLISTTFTGCTSSSDTEIKVN-----PPQFEIVDVGILYL 49
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 94 CVPRRCVLPYTFQFSVKEDYISLQDRDLSTHLVPLAQHVQPPPKDISPSGS--DHF 151
QY 50 YLQWQPPPL---SLDHFKECTVEYELKYNIGSETWKTITIKNLHYKDFDLNKGTEAKIH 106
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 152 LLKWSVPLGDAQVSLLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWLTLEPK 203
QY 107 TLLP-----WQCTNGSEVQ---SSWAETTWISQGPETKQVDMDCVYNNQYLL 154
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

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Db 204 LFLPNSIIVARVRAQLAPGSSLSGRSPGWSPEVHWDSPTE-DKARPQNLOCFDGIQSLN 262
Qy 155 CSWPGIGVLLDTNLYFWYEGLDHALQCYDYIKADQONIGCRFPYLEASDYKDFYICV 214
Db 263 CSWEVWTKVTDVSFGLFYSSPRAGEKKSPVKE-----LQASRYTRYHCSL 311
Qy 215 NGSSENKPIRSYFTFLOQ-----NIVKPLPP-VYLTFTRRESSCEIKLWSIPL 262
Db 312 NVSD---PAHSQVTVSVKRLQKGFIEFNFHQNPNPTLNTKNRDS---YSLHWETQK 365
Qy 263 GPIPARCFDYELIR-----EDDTLLTAIVENETYLTKTNETROLCFVVRSKVNIYC 316
Db 366 MSYPIQHAFOVQYKKLDRWEDSKT-----ENLNAHSMOLPQLEPGTSYCARVRVKTIP 421
Qy 317 SDDGIWSEWSDKQCV 331
Db 422 EYKGLWSEWSNECTW 436

RESULT 15

Q921A0 PRELIMINARY; PRT; 890 AA.
AC Q921A0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR BETA CHAIN.
GN IL5
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Logsdon N.J., Graham A., Scott C.W.;
RT "Guinea pig IL5 receptor beta chain."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94688; AAC77520.1; -;
DR InterPro; IPR000276; -;
DR InterPro; IPR001777; -;
DR InterPro; IPR002996; -;
DR InterPro; IPR003531; -;
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN 1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 890 AA; 96578 MW; D43FB1CA88525536 CRC64;

Query Match 8.48; Score 159.5; DB 11; Length 890;
Best Local Similarity 24.18; Pred. No. 5e-06;
Matches 81; Conservative 47; Mismatches 135; Indels 73; Gaps 19;
Qy 34 PQQPEIVDPGYLYLQWOPPLSLDH---FKECTVEYELKYRNGSETWKTITKNLH 90
Db 138 PPQDVQINTSG--DOVLTWVALEGPHTSWLSQRLDEFEVYKRL-HEPWESAST--LH 192
Qy 91 YKDG-----FDLNGKIEAKIHTLLPWQCTNGSEVQ---SSWAETTYWISPOGIPETK 139
Db 193 SNSQAALGPELFLPSSSTYVARVTRL---ARGSGFGSPQNSPEVSWSSQPG-DQAQ 247
Qy 140 VQDMCVYNNQYLLCSKPKGIGVLLDTNLYFWYEGLDHALQ-CVDYIKADGONI--- 195
Db 248 PQLQCVFDGARTLSCSWEVRSQVTSYSSVGLFY-RSSLDAEGECPCQVQKEELHDYTR 306
Qy 196 -GCRPPYLEASDYKDFYICVNGSENKPIRSYFTFLOQNIYKPLPPVYLTFTRRESSCEI 254
Db 307 HSCQIRVSNRPHSQSYTVVPRNCEKFIrsa-----NHIQMAAPT-LNVTKDGD-TY 357
Qy 255 KIKWSIPGLPIPARCF-----DYEIEIREDDTTLVATVENETYLK----- 296
Db 358 SLRW-----VTEKMYSHIENTFEIQYR---TAGDRWENSKTETLKAHNMPLPPLPE 407

Oy 297 -TTNETROLCFVVRSKVNIYCSDDGIWSEWSDKQCV 331
Db 408 ATTYLAR-----VRVKPSPGAYNGINWSESEQRW 438

Search completed: September 1, 2001, 19:15:54
Job time: 526 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:53 ; Search time 43.66 Seconds
(without alignments)
649.036 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372
Perfect score: 2056
Sequence: 1 MAFVCLAIGCLYFLISTTF.....ILVIFVTGLLLRKPNPKM 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 310.5 | 15.1 | 420 | 2 S21052 | interleukin-5 rece |
| 2 | 292 | 14.2 | 335 | 2 A40267 | interleukin-5 rece |
| 3 | 261 | 12.7 | 831 | 2 JQ1655 | prolactin receptor |
| 4 | 241 | 11.7 | 415 | 2 S12357 | interleukin-5 rece |
| 5 | 220 | 10.7 | 369 | 2 A42565 | interleukin-2 rece |
| 6 | 216.5 | 10.5 | 830 | 2 I50455 | prolactin receptor |
| 7 | 212.5 | 10.3 | 369 | 2 I49280 | interleukin-2 rece |
| 8 | 208 | 10.1 | 373 | 2 A55718 | interleukin-2 rece |
| 9 | 195 | 9.5 | 878 | 2 A40091 | interleukin-3 rece |
| 10 | 180.5 | 8.8 | 897 | 1 A39255 | cytokine receptor |
| 11 | 178 | 8.7 | 896 | 2 I56563 | interleukin-3 rece |
| 12 | 173.5 | 8.4 | 896 | 1 A35782 | cytokine receptor |
| 13 | 165 | 8.0 | 310 | 2 A29884 | prolactin receptor |
| 14 | 165 | 8.0 | 412 | 2 A41070 | prolactin receptor |
| 15 | 165 | 8.0 | 581 | 2 I45971 | prolactin receptor |
| 16 | 165 | 8.0 | 610 | 2 A34631 | lactogen receptor |
| 17 | 165 | 8.0 | 610 | 2 A36116 | prolactin receptor |
| 18 | 159 | 7.7 | 292 | 2 I77525 | prolactin receptor |
| 19 | 159 | 7.7 | 303 | 2 I77524 | prolactin receptor |
| 20 | 159 | 7.7 | 608 | 2 I53269 | prolactin receptor |
| 21 | 151 | 7.3 | 622 | 2 A40144 | prolactin receptor |
| 22 | 150.5 | 7.3 | 917 | 2 I49699 | glycoprotein 130 - |
| 23 | 149 | 7.2 | 616 | 2 A30304 | prolactin receptor |
| 24 | 142.5 | 6.9 | 400 | 2 S06945 | granulocyte-macrop |
| 25 | 138 | 6.7 | 378 | 2 A40266 | interleukin-3 rece |
| 26 | 134.5 | 6.5 | 1097 | 2 S17308 | leukemia inhibitor |
| 27 | 133.5 | 6.5 | 333 | 2 S13684 | granulocyte-macrop |
| 28 | 133.5 | 6.5 | 378 | 2 S50040 | granulocyte-macrop |
| 29 | 131.5 | 6.4 | 630 | 2 I51086 | prolactin receptor |

30 129 6.3 150 2 B34631
31 126.5 6.2 918 2 A36337
32 122.5 6.0 286 2 S50039
33 120.5 5.9 771 2 B38252
34 120.5 5.9 783 2 JH0329
35 120.5 5.9 863 2 C38252
36 112.5 5.5 1630 2 C41214
37 111.5 5.4 1557 2 D41214
38 110 5.4 6805 2 S20901
39 109.5 5.3 918 2 A44257
40 109.5 5.3 26926 1 I38344
41 107.5 5.2 638 2 A33991
42 107.5 5.2 837 2 A34898
43 106 5.2 634 2 S33339
44 105.5 5.1 1825 2 T32828
45 104.5 5.1 1092 2 JX0312

lactogen receptor
membrane glycoprot
granulocyte-macrop
granulocyte colony
granulocyte colony
granulocyte colony
protein-tyrosine-p
protein-tyrosine-p
titin - rabbit (fr
interleukin-6 sign
titin, cardiac mus
somatotropin recep
granulocyte colony
somatotropin recep
hypothetical prote
differentiation-st

ALIGNMENTS

RESULT 1
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C:Accession: S21052; S21050; S21053; A46175; S78106; S78107
R:Murata, Y.; Takaki, S.; Migoita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815
A:Accession: S21052
A:Molecule type: DNA
A:Residues: 1-420 <MUR>
A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A:Experimental source: clone lambda h5R.12
A:Accession: S21050
A:Molecule type: DNA
A:Residues: 1-395, 'I' <MU2>
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A:Experimental source: clone lambda h5R.27
A:Accession: S21053
A:Molecule type: mRNA
A:Residues: 1-332, 'K' <MU3>
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A:Experimental source: clone lambda h5R.25
R:Ravennier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum
A:Reference number: A46175; MUID:92357767
A:Accession: A46175
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 333-420 <TAV>
A:Experimental source: HL-60 cells and eosinophils
A>Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R:Murata, Y.
submitted to the EMBL Data Library, July 1991
A:Reference number: S78106
A:Accession: S78106
A:Molecule type: DNA
A:Residues: 1-128, 'I' <MUW>
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R:Murata, Y.
submitted to the EMBL Data Library, September 1991
A:Reference number: S78107
A:Accession: S78107
A:Molecule type: mRNA
A:Residues: 1-128, 'I' <MU4>
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <NAT>

A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; MUID:91092260
A:Accession: S12357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <TAK>
A:Cross-references: GB:D90205; NID:g220465; PIDN:BAAL4231.1; PID:g220466
C:Keywords: cytokine receptor; transmembrane protein

Query Match 11.7%; Score 241; DB 2; Length 415;
Best Local Similarity 24.9%; Pred. No. 1.1e-11;
Matches 88; Conservative 65; Mismatches 144; Indels 56; Gaps 17;
Qy 34 PQDPEIYDPGVLGYLQWQPLSLDFHFKCTVEYELKYNIGSETWTKITIKNLHYKD 93
Db 29 PVNVTIKATG-LAQVLLHWDNPDEQ-RHVDLEHYHKINAPQDEVDTRKTES---KC 83
Qy 94 GFDLNGIEAKIHTLLPQWCTNGSEVQSWAETTYWISPOGIPETKVQDMDCVYIN---- 149
Db 84 VTPLEHGEFAASVRTILK---SSHTTLASSWVSAEL-KAPPGSPGTSVNTLCTTHTVYSS 139
Qy 150 -----WQY-LLCNKPGLGVLLDNYNLFYWEGLDHALQCVDIK-ADGONICRPP- 200
Db 140 HTHLRPYQVSLRCTLWLGKDAPEDTQYLYYRFGVLTE--KCQEYSRDALNENTACWEP 197
Qy 201 -YLEASDYKDFYICVNGSENKPIRSSYFTQLOINIVKPLPPVLTFTRESSCEIKLWKS 259
Db 198 TFINGKGFQALVHNGSKRAIRPFOLFPLAIDQVNPNNVTEIES-SLYIQWE 256
Qy 260 IPLGPIPARCFDYEIEIREDD-----TTLVATVENETVTLTKTNETROLCFV 308
Db 257 KPLSAPPDHCNFYELKIYNTKNGHIQKELIANKISKIDOVSTYSIQ-----V 305
Qy 309 RSKVNIYSDGGINSEWSKQCEGEDIKTLTLLRFW----LPGFIIILVIF 357
Db 306 RAAVSSPCRMGRGWEWS-OPIYVGKE--RKSLEVE-WHLIVLPTAACFVLLIF 354

RESULT 5

A42565
Interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A42565; A46591; I54332
R:Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.;
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: GB:D11086; NID:g303611; PIDN:BAAL1857.1; PID:g219890
A:Experimental source: MOLT beta lymphoid cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109167)
J. Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He
Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-link
A:Reference number: I54332; MUID:94004847
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>

A:Cross-references: GB:L19546; NID:g349631; PIDN:AAAC37524.1; PID:g349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:I34807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A:Note: defects are associated with an X-linked form of severe combined immunodeficie
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.7%; Score 220; DB 2; Length 369;
Best Local Similarity 25.5%; Pred. No. 4.6e-10;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;
Qy 97 LNKGIEAKIHTLLPQWCTNGSE-VQSSNAETTYWISPOGIPETKVQDMDCVYINQYLLC 155
Db 19 LGVGLNTILT-----PNEGDDTTADFFLTMTPTDSLSVSTLPLPEVOCFVFNVEYMC 72
Qy 156 SW-----KPGIGVLLDNYNLFYWEGLDH--ALQCVDIKADQNIGCRPPYLEASDY 207
Db 73 TWNSSEFQP-----TNLTLYHWYKNSDNDKVQKSHYLFSEITSCQLOKKEIHL 125
Qy 208 KDFYICVNGSENKPIRSSYFTQLOINIVKPLPPVLTFTRESSCEIKLWKSIPGLPIA 267
Db 126 QTFVYVOLQDPRE--PRQATQMLKQLNVLIPWAPENLTLHLKLSOLELNNW---NRELN 180
Qy 268 RCFDYEIEIREDD-DTTLVTATVE-NETVTLTKTNETROLCFVVRKVNLYCDDGIWSEW 325
Db 181 HCLEHLVQYRTDWDHSTQSVYDRHKFSVSDVQCKRYTFRVRSFNPLCSCAQHSEW 240
Qy 326 SDKQCEGEDIKTLTLLRFWLPFGFIIILVIFVTG 360
Db 241 SHPIHW-GSNTSKEN-----PFLFALEAVVISVG 268

RESULT 6

150455
Prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin recepto
A:Reference number: I50455; MUID:94283267
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.5%; Score 216.5; DB 2; Length 830;
Best Local Similarity 24.4%; Pred. No. 2.4e-09;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;
Qy 18 TTFGCTSSSDTEIKVNPQDPEIVDPGVILG-----YLYLQW 53
Db 97 TTYNTVAMNEIGSNSS-----DPQYVDVTSIVQDPVNLSTKTSTASTYLLAKW 150
Qy 54 QPPLSLDHFKCTV-EYELKYNIGSETWTKITIKNLHYKGFDLNKGIEAKIHTLLPWQ 112
Db 151 SPPLADVTSNHHVRYELRLKPEKEWETV---SVGVOTQYKVNRLQAGVKYVQVR 206
Qy 113 CTNGSEVQSSNAETTYWISPOG-IPETKVQDMDCVYINQYLLCCKPGIGVLLDTN 171
Db 207 CVLDIGSEWSSSRHHIIPNGESPPEPTTIKCRSEKETFTCWKPGSGDGHPTNTYL 266
Qy 172 FYWEGLDHALQCVDIKADQNIGCRPPYLEASDYKDFYICVNGSENKPIRSSYFTFQ 231

Db 267 LYSKGESEVPCPDY-KTAGPN-SCYEDKKHTSWTIYNIIVKATNETIGSNVSDPLYVD 324
QY 232 LONIYKPLPPVYLITFRSSCEIK-----LKWS-IPGLPIPA--RCFDYEIEIRDDTLV 284
Db 325 VYIIVOTDPPNVNVTLELKKTKVNRKPYLVTWSPPLADVRSGWLTLDELRLKPEEA--- 381
QY 285 TATVENETVTLKTTNETRQLCFV---RSKNVIYCSDD--GIWSEWS-DKOCWEGEDLS 337
Db 382 -----EEWETIVGQOYHKWFSNPGKKYIVQIHCKPDHGSWSEWSLEKYLQIPTDPR 436
QY 338 KKTLLRFLWLPFGIFILLVIFV 358
Db 437 IKDMV-VMIIVGLSLICLV 456

RESULT 7
I49280
Interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R:Cao, X.; Kozak, C.A.; U.S.A. 90, 8464-8468, 1993
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gene
A:Reference number: A47514; MUID:93391374
A:Accession: I49280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:Cross-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350
A:Accession: A47514
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE>
A:Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of function
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUM>
A:Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.G.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal location
A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2Rgamma

A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta
eptors
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TMM>
F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 10.3%; Score 212.5; DB 2; Length 369;
Best Local Similarity 26.9%; Pred. No. 1.8e-09;
Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;
QY 136 PETKVQDMDCVYVWYLLCSW---KPGIGVLLDTNLYFWYEGDLHAL--OCVDYIK 189
Db 53 PTLPLPEVOCVFNFIEYMNCTWNSSEPOA-----TNLTLYRYKVSNNTFQEGSHYLF 107
QY 190 ADGQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLQNIKVPPLPPVLTFTRE 249
Db 108 SKEITSGCQIQKEDIQLYOTFVVL--QDPQKPORRAVOKLQNLVIPRAPENLTLSNL 165
QY 250 SSECILKWSIPLGPIPARCFDYEIEIREDDTLVTATVENE-TYTLKTTNETRQLCFV 307
Db 166 SESOLELRWK--SRHIKERCLQYLQYRSNRDRSWTEILIVNHEPRFSLPSVDELKRYTFR 223
QY 308 VRSKVNICYDDGISEWSEKQCEG-----EDLSKTKTLRFLWLPFGF--ILILVIFVTGL 361
Db 224 VRSRYNPICGSSQKWSQVPHWGHSHVVENPSLFALEAVLIPVGTMLITLIFVYCW 283
QY 362 LLRKPNYTP 370
Db 284 LERMPPIPP 292

RESULT 8
A55718
Interleukin-2 receptor gamma chain precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
C:Accession: A55718
R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
Genomics 23, 69-74, 1994
A:Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combi
A:Reference number: A55718; MUID:95130114
A:Accession: A55718
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <HEN>
A:Cross-references: GB:U04361; NID:g517411; PIDN:AAC48403.1; PID:g517412
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication

Query Match 10.1%; Score 208; DB 2; Length 373;
Best Local Similarity 26.0%; Pred. No. 4.2e-09;
Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;
QY 115 NGSE-----VQSSWATTTWISPOGIPETKVQDMDCVYVWYLLCSW-----KPGI 161
Db 31 NGNEDITPDDFLTATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSEPRP-- 82
QY 162 GVLLDTNLYFWYEGE--DHALQCVDIKADGQNGICRFPYLEASDYKDFYICVNGSSE 219
Db 83 -----TNLTLYRYKVSNNTFQEGSHYLFPSREYTAGVQLQKEEHLHYETFWQLDRPE 137
QY 220 NKPIRSSYFTFQLQNIKVPPLPPVLTFTRESCEIKLWSIPLGPIPARCFDYEIEIREDD 279
Db 138 --PRRQSTQKLQNLQNLVIPWAPENLTLSNLSQLELSWS---NRHLDHCLHEVHVQYRSD 192

```
QY 280 -DTTLVATVEN-ETVTLKTTNETQLCFVRSKVNIVCSDDGIWSEWSDKOCWEGEDLS 337
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 193 WDRSWTEQSDVHNSFSLPSVQCFYFVRVSRYNPLCGSAQRWSEWSPHFW-GSNWTS 251
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 338 KXTLL---RFFWLPGFILLIVFV 358
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 252 KENPLFASEAVLPLGSMGLIISLI 276
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |

RESULT 9
A40091
A:Title: Interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022
R:Ritoh, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I.
  Science 247, 324-327, 1990
A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
A:Reference number: A40091; MUID:90117145
A:Accession: A40091
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <I>
R:Gorman, D.M.
  submitted to GenBank, November 1989
A:Reference number: A43022
A:Accession: A43022
A:Molecule type: mRNA
A:Residues: 1-815, 'Q', 817-878 <GOR>
A:Cross-references: GB:M29855; NID:g198342; PID:g309406
C:Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains
  receptors.
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-878/Product: interleukin-3 receptor beta chain #status predicted <MAT>
F:23-440/Domain: extracellular #status predicted <EXT>
F:239-236/Domain: cytokine receptor homology <CRS1>
F:254-433/Domain: cytokine receptor homology <CRS2>
F:441-462/Domain: transmembrane #status predicted <TM>
F:463-878/Domain: intracellular #status predicted <INT>

Query Match 9.5%; Score 195; DB 1; Length 878;
Best Local Similarity 24.1%; Pred. No. 1.3e-07;
Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

QY 34 PPQDFIVDPGLYLYLQWQPL---SLDHFKECTVEYELKYRNIGSETWTKITIKNLH 90
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 139 PKDIIHISPG--DHFLEWVSGLGSQVSWLSSKDIIEVAYKRL-QDSWED--ASSLH 193
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 91 YKDGFDLNGIEAKIHTLP-----WQCTNGSEVQ---SSWAETTYWISPOGIPET 138
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 194 -TSNFOVN--LEPKL--FLPNSIYAARVTRLSAGSSLSGRPSRWSPEVHDSQPG-DKA 247
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 139 KYQDMCVYNNQYLLCSKPKGIGVLLDNYNLFYWEGLDHALQCVDIKADQNI--- 195
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 248 QPNQLQCFDGIQSLCHSEVNTQTGVSFGLFYRPSAARPEKCSPPVQKQASVYTR 307
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 196 -GCRFPYLEADYKDFYICVNGSSENKPIRSSYFTFQQLNIVKPLPPVY-LFTTRESSCE 253
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 308 YRCSLPVPPEPSAHSQVTSVKHLEQCKFI-MSYHIQME-----PPILNQTKNRDS--- 357
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 254 IKLKSIPGLPIPARCFD--YEIETREDTTLVATVEN-----EYTLKTTNETQLCFV 307
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 358 YSLHWETQKIP---KYIDHTFQVQYKKKSEWKSNDKTENLGRVNSMDLPQLPEPDTSYCAR 414
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 308 VRSK-VNIVCSDDGIWSEWSDKOCWEGEDLSKKTLLRFLWLPFGFILLIVFTGLL 363
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 415 VRVKPISDY---DGIWSEWSENYTWT-TDWNVPTL---WI-----VLILVFLIFTLL 460
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
```

```
RESULT 10
A39255
A:Title: cytokine receptor common beta chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C:Accession: A39255
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
  Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-
  A:Reference number: A39255; MUID:91088571
A:Accession: A39255
A:Molecule type: mRNA
A:Residues: 1-897 <HAY>
A:Cross-references: GB:M38275
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-speci
  C:Genetics:
A:Gene: GDB:CSF2RB
A:Cross-references: GDB:I26838; OMIM:138981
A:Map position: 22q13.1-22q13.1
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane prote
  F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-897/Product: cytokine receptor common beta chain #status predicted <MAT>
F:17-443/Domain: extracellular #status predicted <EXT>
F:35-232/Domain: cytokine receptor homology <CRS1>
F:250-431/Domain: cytokine receptor homology <CRS2>
F:444-460/Domain: transmembrane #status predicted <TM>
F:461-897/Domain: intracellular #status predicted <INT>

Query Match 8.8%; Score 180.5; DB 1; Length 897;
Best Local Similarity 22.6%; Pred. No. 2e-06;
Matches 90; Conservative 58; Mismatches 146; Indels 105; Gaps 21;

QY 32 VNPPQDFEIVDPGLYCY-----LYLQWQP-----LSLDHF----- 62
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 97 VIPCOSFVVTDVDFSFQDRPLGLTRLVTLAQHVQPPPEPRDLQISTDQDHFLLTWSVAL 156
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 63 -----KECTVEYELKYRNIGSETWK--TITKLNHYKDGFDLNGKTE-----A 103
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 157 GSPQSHWLSFGDLEFEVYKRL-QDSWEDAAILLNNTS-----QATLGFELHMLPSTYYA 210
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 104 KIHT-LLPWOCTNGSEVQSSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSKPKGIG 162
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 211 RVRTLAPGSRSLGR--PSKWSPEVCWDSPG-DEAQPNLECFDGAALVSCSWEVRKE 267
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 163 VLLDTNYNLFYWEGLDHALQCVDIKADQNI-----GCRFPYLEADYKDFYICVN 215
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 268 VASSVSFGIFYKPSPDAGEECSPVLR---EGLGSLHTRHCOIPVDPDPATHGQYIVSVQ 324
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 216 GSSENKPIRSSYFTFQQLNIVKPLPPVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIE 275
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 325 PRRAEKHKSSV-----NI--QMAPPSLNVTKDGD-SYSLRWETMKMYEHLDTFTFQ 375
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 276 IREDDTTLVAT-VENETVTLKTTN-----ETRQLCFV-VRSKVNIVCSDDGIWSE 324
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 376 YRKD-----TATWKSKTETLQNAHSMALPALEPSRYWARVVRVTRTGY---NGIWESE 427
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
QY 325 WSDKQOCWEGEDLSKKTLLRFLWLPFGFILLIVFTGLL 363
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 428 WSEARSWDTESV-----LPMWYALIVFLTAVL 457
      | : : : : : | : : : | : : | : : | : : | : : | : : | : : |

RESULT 11
I56563
A:Title: interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
  J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia a
  A:Reference number: I56563; MUID:95370942
```

Query Match 8.4%; Score 173.5; DB 1; Length 896;

```
RESULT 14
A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000
C:Accession: A41070; I55417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin
A:Reference number: A41070; MUID:92041834
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390
R:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
A:Reference number: I55417; MUID:95014432
A:Accession: I55417
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964
A:Experimental source: Nb2-11C cell line
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match      8.0%; Score 165; DB 2; Length 412;
Best Local Similarity 28.5%; Pred. No. 1.3e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

QY 131 SPQGIPEKVDMDCVYNNQYLCSWKPGLVLDNTNLYFWYEGLDHALQCVDYIKA 190
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 SPQGIPEKVDMDCVYNNQYLCSWKPGLVLDNTNLYFWYEGLDHALQCVDYIKA 190
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 191 DGQNGICRFPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQIQNIKVPPLPPVILT 245
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 SGPN-SCFESKQYTSIWKIYITVATNQMGSSSDPL-----YVDVYIYVEPEPRNLT 129
    : : : ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 246 F----TRESSCEIKLWSP-IGPIPARCFDYIEIREDDTTLVATVENETITLKTNE 300
    : : : ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 LEVKQLDKKTYLWVKSPTITDVKTFWTFEYR-----LKPEAEWEIHTGCH 182
    : : : ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 TRQL-----CFVRSKVNIIYSDDGINSWSDKQWE 332
    | : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 QTFKVFDPGQKYLQVTRCK---PDHGYSRWSQESSVE 220
    | : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>
```

Query Match 8.0%; Score 165; DB 2; Length 581;

```
Best Local Similarity 31.3%; Pred. No. 1.9e-05;
Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;

QY 136 PETKVQDMDCVYNNQYLCSWKPGLVLDNTNLYFWYEGLDHALQCVDYIKADGONI 195
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 PPEKPLVKCRSPGKETTCWWEPCADGGLPTNYITLVHKEGETLIHECPDY-KTGGPN- 84
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 196 GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQIQNIKVPPLPPVILTFTRESSCEIK 255
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 SCYFSKKHTSIWKMYVITVNAINQMGISSDDPLYVHVTVIVEPEPPANLTLELKHPEDRK 144
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 ----LKWSIP-LGPIPARCF--DYIEIREDDTTLVATVENET-YTLKTTN-ETRQLCF 306
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 PYLWIKWSPPTMDYKSGWFIQYIEIRLKPKEAT-----DWETHFTLKQTLKIFNLYP 198
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 307 VVRSKVNIIYCS-DDGIIWSEWS 326
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 GQKYLQVQINCRPDHGYWSEWS 219
    ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: September 1, 2001, 19:07:54
Job time: 121 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:15:52 ; Search time 68.62 Seconds
(without alignments)
717.247 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372

Perfect score: 2056

Sequence: 1 MAFVCLAIGCLYTLISTTF.....ILVIFVTRLRLRPNTYPRM 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1194.5 | 58.1 | 383 | 11 | O88786 |
| 2 | 310.5 | 15.1 | 420 | 4 | Q14633 |
| 3 | 309.5 | 15.1 | 396 | 4 | Q14631 |
| 4 | 292 | 14.2 | 333 | 4 | Q15469 |
| 5 | 291.5 | 14.2 | 415 | 11 | Q920K4 |
| 6 | 264.5 | 12.9 | 349 | 6 | O97597 |
| 7 | 241.5 | 11.7 | 279 | 4 | O9UDY5 |
| 8 | 197.5 | 9.6 | 363 | 13 | O9DE01 |
| 9 | 185.5 | 9.0 | 611 | 13 | O9PTI0 |
| 10 | 185.5 | 9.0 | 611 | 13 | O9IBR6 |
| 11 | 178 | 8.7 | 896 | 11 | Q64146 |
| 12 | 173.5 | 8.4 | 881 | 13 | O57519 |
| 13 | 172 | 8.4 | 611 | 13 | O9PTB9 |
| 14 | 170 | 8.3 | 890 | 11 | Q9Z1A0 |
| 15 | 167 | 8.1 | 622 | 6 | Q9N0J7 |
| 16 | 165 | 8.0 | 296 | 6 | O18880 |
| 17 | 164 | 8.0 | 227 | 6 | O9GLW3 |
| 18 | 159 | 7.7 | 581 | 6 | O46561 |
| 19 | 156 | 7.6 | 625 | 6 | O9XS92 |

| | | | | | |
|----|-------|-----|------|----|--------|
| 20 | 153.5 | 7.5 | 918 | 13 | Q9W609 |
| 21 | 153 | 7.4 | 217 | 6 | O46386 |
| 22 | 151 | 7.3 | 206 | 4 | Q16354 |
| 23 | 151 | 7.3 | 349 | 4 | Q9UHJ5 |
| 24 | 147.5 | 7.2 | 538 | 13 | Q9DFU0 |
| 25 | 146.5 | 7.1 | 422 | 4 | Q9UHH5 |
| 26 | 145.5 | 7.1 | 422 | 4 | O75462 |
| 27 | 143.5 | 7.0 | 425 | 11 | Q9JM58 |
| 28 | 138 | 6.7 | 390 | 4 | Q9UEH7 |
| 29 | 135 | 6.6 | 346 | 13 | Q93404 |
| 30 | 130.5 | 6.3 | 198 | 6 | O18985 |
| 31 | 126.5 | 6.2 | 329 | 4 | Q9UQ41 |
| 32 | 119.5 | 5.8 | 371 | 4 | Q9HC73 |
| 33 | 117.5 | 5.7 | 896 | 4 | Q13594 |
| 34 | 117.5 | 5.7 | 906 | 4 | Q13593 |
| 35 | 117.5 | 5.7 | 958 | 4 | Q13592 |
| 36 | 116.5 | 5.7 | 1282 | 5 | Q9VWE0 |
| 37 | 114 | 5.5 | 894 | 6 | Q9MYL1 |
| 38 | 114 | 5.5 | 925 | 6 | Q9MYK9 |
| 39 | 114 | 5.5 | 1163 | 6 | Q9MYL2 |
| 40 | 114 | 5.5 | 1194 | 6 | Q9MYL0 |
| 41 | 113.5 | 5.5 | 896 | 4 | O92919 |
| 42 | 113.5 | 5.5 | 958 | 4 | O92920 |
| 43 | 113.5 | 5.5 | 1165 | 4 | Q92921 |
| 44 | 111 | 5.4 | 628 | 11 | Q9JRG1 |
| 45 | 110 | 5.4 | 6875 | 6 | Q28733 |

ALIGNMENTS

RESULT 1

O88786 PRELIMINARY; PRT; 383 AA.

AC O88786; PRELIMINARY; PRT; 383 AA.

DT 01-NOV-1998 (TREMREL. 08, Created)

DT 01-NOV-1998 (TREMREL. 08, Last sequence update)

DT 01-MAR-2001 (TREMREL. 16, Last annotation update)

DE IL-13 RECEPTOR ALPHA 2.

GN IL13RA2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/HEJ; TISSUE=THYMUS;

RX MEDLINE=98391042; PubMed=9725226;

RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,

RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,

RA Collins M.,

RT "The murine IL-13 receptor alpha 2: molecular cloning,

RT characterization, and comparison with murine IL-13 receptor alpha 1.";

RL J. Immunol. 161:2317-2324(1998).

DR EMBL; U65747; AAC33240.1; .

DR MGD; MGI:1277954; IL13ra2.

DR InterPro; IPR002996; .

DR InterPro; IPR003332; .

DR PROSITE; PS01356; HEMATOPO_REC_SF2; UNKNOWN_1.

SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 58.1%; Score 1194.5; DB 11; Length 383;

Best Local Similarity 58.9%; Pred. No. 1.4e-98;

Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLAIGCLYTLISTTFGCTSSDTEIKVNPDPDFEIVDPGYLYLQWQPLSLD 60

DB 1 MAFV--HIKCLFILLCTTGYS----LEIKVNPDPDFEIVDPGYLYLQWQPLSLD 54

QY 61 HFKECTVEYELKYNIGSETWTKTITIKNHYKDGDFLNKGIEAKIHTLFPWCTNGSEVQ 120

DB 55 KFKGCTLELAYRNVDSDSWKTIITRNLYKDGDFLNKGIEKIRTHLSECTNGSEVQ 114


```
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 12.9%; Score 264.5; DB 6; Length 349;
Best Local Similarity 24.4%; Pred. No. 1.2e-15;
Matches 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;

QY 53 WOPPLSLDFHFKCTVYELKYRNIQSGTWKTIITKLNHYKDGFDLNGKTEAKIHTLLPQ 112
DB 18 WNPPEGAS--PNCSLAY---FSHFGNKQDKKAPET-HRSKEVPLNERICLVQGS-----Q 67

QY 113 C-TNGSEVOSSWAETTYWISPOGIPETKYVODMDCVYNNQYLLCSWKPGIGVLLDTNLYL 171
DB 68 CSTNESEKPSILVEKCF-SPPEGDPESAVTALQCIWHLNRYKMKCTWLPGRNASPDNPYIL 126

QY 172 FYWYEGDLHALQCVYIKADQGNICRFPYLEASD--YKDFYICVNGSSSENKPIRSSFT 229
DB 127 YVHNSLKGILQCNFYR-EGHIAACSFNLTKVKDSSFEQHSVQVMVRDNAGKISPSFNI 185

QY 230 FOLQNVKPLPPVYLTFTRESSECEIKLWSIPLGPIPARCFDYEIREDDTTLVTATVE 289
DB 186 VPLTSHVKP-DSHIKLNLSFQGLYVQWTFNQF-QFSQCLCYEVEVINSHA----- 235

QY 290 NETYILKTTNTR-----QLCFV-----RSKVNICY-SDDGIWS 323
DB 236 -ETHIDFYVEEAKQCNTEPEGNLEGTICPMVGPLPDTLNTVIRVKTNKLCEYEDDKLWS 294

QY 324 ENSDKOCWEGEDLSKTLRLFWLPGFILLILVFTGLLL 363
DB 295 NWS-----QAMSIGOKANOTFYIT--TLLIIPVIAAAVI 327

RESULT 7
QYUDY5 PRELIMINARY; PRT; 279 AA.
AC QYUDY5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81380; AAD00511.2;
DR HSSP; P40189; 1BQU.
DR InterPro; IPR002996;
DR InterPro; IPR003532;
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;

Query Match 11.7%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 1e-13;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;

QY 11 LYTLFLISTFGCTSSSDTEIKVNPQDPFVIDPGVGLYILQWQPPSLDHFKECTVEY- 69
DB 10 LWALLCAGGGGGGAAPTETQPPVTNLSVSNLCIVITWNPPEGAS--SNCSLNYF 67

QY 70 ----ELKRYNTGSETWKTITIKNLHYKDGFDLNGKTEAKIHTLLPQ-C-TNGSEVOSSWA 124
DB 68 SHFGDKQDKKIAPESTRSI-----EVLNERICLVQGS-----QCSTNESEKPSILV 114

QY 125 ETTYWIS-POGIPETKYVODMDCVYNNQYLLCSWKPGIGVLLDTNLYNLYWYEGDLHALQ 183
DB 115 EKC---ISPPEGDPESAVTELOQCIWHLNLSYKMKCSMLPGRNTSPDNTYLYWHRSLERIKH 172
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QY 184 CVDYIKADQGNICRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFTQLQNIYKPLPP 241
DB 173 C-ENTFREGQYGCFSFDLTKVKDSSFEQHSVQIMVKDNAGKIRPFENIVPLTSRVKPDPP 231

QY 242 --VYLTFTRESSECEIKLWSIPLGPIPARCFDYEIREDDT 281
DB 232 HIKNLSFHD--DLVQWENPQNF-SRCLFYEVEVNSQT 269

RESULT 8
QYDEQ1 PRELIMINARY; PRT; 363 AA.
AC QYDEQ1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OC Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RA Wang T., Secombes C.J.;
RL "Cloning and expression of the first non-mammalian cytokine receptor
common gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1;
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 363 AA; 41861 MW; DF69B2EE3EEA06D3 CRC64;
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Query Match 9.6%; Score 197.5; DB 13; Length 363;
Best Local Similarity 21.9%; Pred. No. 1.2e-09;
Matches 61; Conservative 56; Mismatches 134; Indels 27; Gaps 9;

QY 97 LNKGEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKYVODMDCVYNNQYLLCS 156
DB 1 IHKYRVELVTLLIPIVHIDMKMGWS--LFLLSLQGYEAPSTPNVNCILINDYVNCI 58

QY 157 WKPGLVLLDTNLYNLYWYEGDLHALQCVYIKADQGNICRFPYLEASDYKDFYICVNG 216
DB 59 WSE--QSIPEVNTFTFSRFFIKDNMEECTYLOESYAVGCLSDYKSDRFR----- 108

QY 217 SSENKPIRSSYFTFO---LQNVKPLPPVYLTFTRESSECEIKLWSIPLGPIPARCFDY 273
DB 109 TLKTKLVHQNMSYVQDHNLSKLVKPPVNLSEVMKDPENLYWNNSKNTF---CIESE 165

QY 274 IEIREDDTTLVTATVENE-TYTLKTTNETRQLCFVVRKVNLYCSDDGIIWSEWSKQWE 332
DB 166 VYRINSKDKWKTSTPSEKQYAVAFPLKSSRYEFQVRAVNDMCGSEFSEFSEWSQPIQWD 225

QY 333 G-----EDLSKKTLLRFWLP-FGFILILVIFVTGLL 363
DB 226 SMKGNITDISGSS-MSVWKPVLSLVGTTFLILACML 262

RESULT 9
QYPTIO PRELIMINARY; PRT; 611 AA.
AC QYPTIO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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RN SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL; AF193800; AAF05776.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629F9F1776FFB6 CRC64;

Query Match          9.0%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY 127 TVWISPGIPETKQVDMDCVYNNWQYLLCSWKPGLVLDNTNLFYWYEGDLHALQCV 186
Db 22 TVSLNAQSLPGKPVID-KCRSEKVTFTSCWKPGLVLDNTNLFYWYEGDLHALQCV 80
QY 187 YIKADGONIGCRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQNI 239
Db 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVYVATNALGNSVDEESVDITY-----IVQ 131
QY 240 PPVLTFTRESS-CEIKLKWISPLGIPARCFD-----YEIEIRDDTTLVTATVE 289
Db 132 PTNVSLAVESGHDLKLLK-----LPPAMVDVQSGWLTLYEYVYKEEKEQWEAHL 185
QY 290 NETYTLKTTNETRQLCFVVRKSNVNYCS-DDGIWSEWSKQWEGEDLSKTLRLFWLP 348
Db 186 GNQLKLFGLTPGGNVVQ-----VRCKPDSGHSEWSESTYIPIGGGKTDLTWISI 241
QY 349 GFILLIVIFVT 359
Db 242 G-ALSAVICLT 251

RESULT 10
Q9IBF6 PRELIMINARY; PRT; 611 AA.
AC Q9IBF6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
RT "Cloning of a cDNA for Xenopus prolactin receptor and its
RT metamorphic expression profile.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030443; BAA90400.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

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Query Match          9.0%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY 127 TVWISPGIPETKQVDMDCVYNNWQYLLCSWKPGLVLDNTNLFYWYEGDLHALQCV 186
Db 22 TVSLNAQSLPGKPVID-KCRSEKVTFTSCWKPGLVLDNTNLFYWYEGDLHALQCV 80
QY 187 YIKADGONIGCRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQNI 239
Db 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVYVATNALGNSVDEESVDITY-----IVQ 131
QY 240 PPVLTFTRESS-CEIKLKWISPLGIPARCFD-----YEIEIRDDTTLVTATVE 289
Db 132 PTNVSLAVESGHDLKLLK-----LPPAMVDVQSGWLTLYEYVYKEEKEQWEAHL 185
QY 290 NETYTLKTTNETRQLCFVVRKSNVNYCS-DDGIWSEWSKQWEGEDLSKTLRLFWLP 348
Db 186 GNQLKLFGLTPGGNVVQ-----VRCKPDSGHSEWSESTYIPIGGGKTDLTWISI 241
QY 349 GFILLIVIFVT 359
Db 242 G-ALSAVICLT 251

RESULT 11
Q64146 PRELIMINARY; PRT; 896 AA.
AC Q64146;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3R<BETA>.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo.";
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; S79263; AAB35068.1; -.
DR EMBL; AJ000555; CAA04186.1; -.
DR InterPro; IPR000282; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003531; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Signal.
FT NON_TER 1
FT NON_TER 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288AA1052 CRC64;

Query Match          8.7%; Score 178; DB 11; Length 896;
Best Local Similarity 21.4%; Pred. No. 2e-07;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLAIGCL--YT-FLISTTTCGCTSSSDTEIKVN-----PPQDFEIVDPGLVGL 49
Db 94 CVPRRCVLTQFSVKEDYISLQPDRLSIHLVPLAQHVQPPPKDISPSG--DHF 151

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RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ272217; CAB75847.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003528; -.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 622 PROLACTIN RECEPTOR.
SQ SEQUENCE 622 AA; 69425 MW; 65F9522C6CD6DB6 CRC64;

Query Match 8.1%; Score 167; DB 6; Length 622;
Best Local Similarity 28.8%; Pred. No. 1.2e-06;
Matches 61; Conservative 26; Mismatches 91; Indels 34; Gaps

QY 131 SPOGIPETKVQDMDCVYVNWVLLCSWKGKIGVLLDTNYNLFVWYEGLDHALQCVDYIKA 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 26 SPPGKPEI-----FKCRSPNKEFTFCWWRGADGGLPTNYSLAYHKGEKEFIHECPDYV-T 80

QY 191 DGNIGICRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLQNIWKPLPPVYLFTRES 250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 GGNP-SCHFGKQYTSWRVYIITVNATNEMGSTLSDEIYVDVYIIVEPDPPLNV----- 134

QY 251 SCEIK-----LKWSSIP-LGPIPARCFD--YEIREDDTTLVTATVENETVTLKT 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 -VEVKQPEDKPKPLWIKWSPPTLIDLKTCWFTLLYELQKPNAE-----EWETHFAQG 187

QY 298 TNETQLCFVRSK--VNIYCS-DDGIWSEWS 326
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 188 QTDFKVLSLHPGOKYLVQVRCKPDHGYWSSWS 219

Search completed: September 1, 2001, 19:15:53
Job time: 525 sec

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Search completed: September 1, 2001, 19:15:53
Job time: 525 sec

